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Second 1. Application US/09846329A

Patent No. 6620786

GENERAL INFORMATION:

APPLICANT: Jackowski, George

TITLE OF INVENTION: 0f 2937 Daltons

FILE REFERENCE: 2132.052

CURRENT APPLICATION NUMBER: US/09/846,329A

CURRENT FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 123; DB 4; Length 28; 100.0%; Pred. No. 5.6e-13;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
CUNTX: New Jersey
COUNTXY: USA
ZIP: 07974
                                             US-08-910-041-1
US-09-38-474-1
US-09-100-546-1
US-09-010-715-1
US-09-610-715-1
US-08-803-364-7
US-09-024-198-13
US-08-803-344-7
US-09-024-198-13
US-08-803-344-1
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US-09-024-198-10
US-09-186-409-10
US-08-801-364-6
US-09-024-198-12
US-09-186-409-12
                                   -08-485-938A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 24; Conserv
US-08-153-799-14
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LENGTH: 28
 TYPE: PRT
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                                                                                 August 19, 2005, 10:50:49; Search time 22 Seconds (without alignments) 81.435 Million cell updates/sec
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Sequence 4, 1
Sequence 2, 1
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(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/ReCOMB.pep:*
(cgn2_6/ptodata/1/iaa/ReCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-98-186-2
US-09-949-016-11170
US-08-256-938-2
US-08-256-938-4
US-08-797-689-16
US-09-984-186-16
US-08-134-638-1
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US-08-948-176-1
US-08-762-776-2
US-08-769-746-2
US-08-723-619-3
US-08-897-956A-2
US-09-919-09-977
US-09-919-09-370
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1 DAHKSEVAHRFKDLGEENFKALVL 24
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Maximum Match 100%
Listing first 45 summaries
                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seg leńgth: 200000000
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Match Length
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Sequence 1, Application US/08984176

Barent No. 594869

GREERAL INFORMATION:

APPLICANT: CARTER, DANIEL C

APPLICANT: RUKER, FLORLAN

TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER

FILE REFERENCE: 08/984.176

CURRENT APPLICATION NUMBER: US/08/984,176

CURRENT PILING DATE: 1997-12-03

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 24; Conservative 0; Mismatches 0: Indela
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APPLICANT: Kerry-Williams, Sean M
APPLICANT: Gilbert, Sarah C
TITLE OF INVENTION: Yeast Strains and Modified Albumins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
           CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

NAME: BROAD JR., ROBERT L.

REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: 18,757
REFERENCE/DOCKET NUMBER: 205-544-021
TELEPHAN: 205-544-021
TELEPHAN: 205-544-0258
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids

TYPE: amino acid
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PC-DOS/MS-DOS
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; Sequence 2, Application US/08702572
; Patent No. 5965386
                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 24; Conservative
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ORGANISM: Homo sapiens
  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-448-196A-3
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US-08-984-176-1
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Sequence 3, Application US/08448196A

Sequence 3, Application US/08448196A

GENERAL INFORMATION:
APPLICANT: CARTER, DANIEL C.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
TITLE OF INVENTION: RELATED PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE NASA
STREET: MARSHALL SPACE FLIGHT CENTER
CITY: HUNTSVILLE
STATE: ALABAMA
CONNTRY: USA
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OTHER INFORMATION: /note= "Alternative C-termini of
OTHER INFORMATION: HSA(1-n)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Amino acid sequence of
natural HSA"
                FILING DATE:
CLASSIFCATION: 435
PRIOR APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION NUMBER: US 07/847975
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT INPORMATION:
APPLICATION NUMBER: 24864
REGERENCE/DOCKET NUMBER: 22089
REGERENCE/DOCKET NUMBER: 278832
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 665 2400
TELEPRONE: (908) 771 6159
  APPLICATION NUMBER: US/08/153,799
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 35812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHEICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) LOCATION: 1..585
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-153-799-14
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LOCATION: 369..4
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100.0%; Score 123; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 24; Conservative 0; Mismatches n: Tradala
                                                                                                                                                                                                                                                                                                                                                        Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/0822619
Patent No. 565252
GENERAL INFORMATION:
APPLICANT: Lichenstein, Henri
APPLICANT: Lichenstein, Henri
APPLICANT: Warfel, Mark
APPLICANT: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ANGEN Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
CITY: Thousand Oaks
CONTANTE: California
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 24; Conservative 0; Mismatches 0;
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Patent No. 5707828
GENERAL INFORMATION:
APPLICANT: Sreekrishna, Kotikanyadan APPLICANT: Barr, Kathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER REALPABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 DAHKSEVAHRFKDLGEENFKALVL 48
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                           TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
TOPOLOGY: linear
JOPOLOGY: linear
US-08-746-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: unl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-222-619-3
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Sequence 2, Application US/08769746

Remember No. 627405

GENERAL INFORMATION:
APPLICANT: Sonnenschein, Carlos
APPLICANT: Sonce No. Ana M.
TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: 3
CORRESPONDENCE Medlen & Carroll, LLP
STREET: 220 Monitsomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSING SYSTEM: 105/08/769,746
FILING DATE: 19-DEC-1996
CLASSIFICATION NUMBER: US/08/769,746
FILING DATE: 19-DEC-1996
CLASSIFICATION: 435
CRASHER ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                      COUNTIER READABLE FORM:

EDUNYTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: MicroSoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,572

FILING DATE: 11-NOV-1996

CLASSIFICATION DATA:

APPLICATION NUMBER: W0 95/23857

FILING DATE: 1-MAR-1995

APPLICATION NUMBER: GB 9404270.2

FILING DATE: 1-MAR-1994

ATTONEY/AGENT INFORMATION:

NAME: NAOM: BIGWAR

REGISTRATION NUMBER: 38,384

REGISTRATION NUMBER: GE0114 US

TELEBCOMMUNICATION INFORMATION:

TELEBCOMMUNICATION INFORMATION:

TELEBCOMMUNICATION INFORMATION:

TELEBCOMMUNICATION INFORMATION:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: MBRI-02584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DAHKSEVAHRFKDLGEENFKALVL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610/878/4294
INFORMATION FOR SEQ ID No: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
TOPOLOGY: linear
ESSEE: Centeon L.L.C.
ET: 1020 First Avenue
: King of Prussia
E: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-702-572-2
                                                                                                                                           USA
      ADDRESSEE:
                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-08-769-746-2
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Sequence 977, Application US/09976594

Sequence 977, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
GENERAL INFORMATION:
TYPLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS TILLE REFERENCE: PA-00140 SCURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
PRIOR PELL PROGRAM
SEQ ID NO 9-77

LENGHT. 609
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Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
APPLICANT: Easer, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 370
LIENGTH: 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 123; DB 4; Length 609; 100.0%; Pred. No. 2e-11; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEX: misc feature
OTHER INFORMATION: Incyte ID No. 6727066 088957CD1
US-09-919-039-370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 088957CD1
US-09-976-594-977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 DAHKSEVAHRFKDLGEENFKALVL 48
                                 25 DAHKSEVAHRFKDLGEENFKALVL 48
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PCT-US95-04075-3
; Sequence 3, Application PC/TUS9504075
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Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                      RESULT 10
US-09-976-594-977
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100.0%; Score 123; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 24; Conservative 0; Mismatches 0: Indels C
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APPLICANT: Brierley, Russell A.
APPLICANT: Thill, Gregory P.
APPLICANT: Tachopp, Juerg F.
APPLICANT: TSCHOPP, JUERG F.
TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN TITLE OF INVENTION: PICHIA PASTORIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City
                                                                                                                                                                                                                                                                                       ZIP: 11530-0239

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGERT INFORMATION:
NAME: DiGiglio, Frank
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9108Z
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4366
TELEEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08897956A
Fatent No. 6423512
GENERAL INFORMATION:
APPLICANT: Mary Ellen Digan
APPLICANT: Philip Lake
APPLICANT: Hermann Gram
TITLE OF INVENTION: Fusion Polypeptides
FILE REFERENCE: 600-7244/CPA
CURRENT APPLICATION NUMBER: US/08/897,956A
CURRENT FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/022,689
FRIOR APPLICATION NUMBER: 60/022,689
FRIOR SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DAHKSEVAHRFKDLGEENFKALVL 24
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amino acid
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Best Local Similarity 100.0
Matches 24; Conservative
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LENGTH: 609 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO 2
| LENGTH: 609
| TYPE: PRT
| ORGANISM: Homo Sapiens
US-08-897-9568-2
                                                                                                                                                                                                             CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530-0299
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TELEPHONE: (610) 454-3839
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-984-186-2
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APPLICANT: Fleer, Reinhard
APPLICANT: Fleer, Alain
APPLICANT: Fleer, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Jung, Gerard
APPLICANT: OGNICAL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Score 123; DB 5; Length 609;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: AMGENINC.
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPELICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/256,927
FILING DATE: 28-UUL-1994
APPLICATION NUMBER: FR 92/01064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 DAHKSEVAHRFKDLGEENFKALVL 48
                                                                                                                                                                                   STATE: California
COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DAHKSEVAHRFKDLGEENFKALVL 24
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: WORD 5.1 (PATENTIAL)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08797689
Patent No. 5876969
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
INFORMATION FOR SEQ 1D NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US95-04075-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-797-689-2
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APPLICANT: Fleer, Reinhard
APPLICANT: Fleer, Alain
Guitton, Jean-Dominique
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 123; DB 2; Length 610;
Pred. No. 2e-11;
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION - AUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 23-JAN-1993
ATTORREY/AGRIT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 123; D
Best Local Similarity 100.0%; Pred. No. 2e-
Matches 24; Conservative 0; Mismatches
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P.38,619
REFERENCE/DOCKET NUMBER: 2792006-US
TELECOMMUNICATION INFORMATION:
TELECHAX: (610) 454-3839
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 DAHKSEVAHRFKDLGEENFKALVL 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09984186 Patent No. 6686179 GENERAL INFORMATION:
31-JAN-1992
                                                                                                                                                                                                                                                                                                                     LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-797-689-2
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GENERAL INFORMATION:
APPLICANT: YEA, PALTICE
TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 100.0%; Score 123; DB 1; Local Similarity 100.0%; Pred. No. 2.6e-11; nes 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/256,938
FILING DATE:
CLASSIPICATION 135
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/01065
FILING DATE: 31-0AN-1992
ATTORNEY/AGBNT INFORMATION:
NAME: Goodman, Rosanne
REGISTATION NUMBER: 32.534
REPERBNEK/DOCKET NUMBER: ST92007-US
TELECOMMUNICATION INFORMATION:
TELEPRAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ST92007-US
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STREET: 500 Arcola Road, 3C43
CIIY: COllegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 DAHKSEVAHRFKDLGEENFKALVL 48
                       SOFTWARE: Word 5.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DAHKSEVAHRFKDLGEENFKALVL 24
                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/01065
FILING DATE: 31-0AN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (Patentin)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: ST92(
TELEPHONE: (610) 454-3817
TELEPHONE: (610) 454-3817
INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 783 amino acids
TYPE: amino acid
TOPE: amino acid
TOPE: amino acid
TOPE: amino acid
TOPE: amino acids

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Patent No. 5665863
System 7.1 (Patentin)
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Matches
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Sequence 11170, Application US/09949016

Sequence 11170, Application US/09949016

Sequence 11170, Application US/09949016

Sequence 11170, Application US/09949016

TITLE NEVENTION: POLIYORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/237,768

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03
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Patent No. 5665863

GENERAL INFORMATION:
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: OCCONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYBEPTIDES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STRRET: 500 Arcola Road, 3C43
CITY: Collegeville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 DAHKSEVAHRFKDLGEENFKALVL 48
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TYPE: amino acid
   454-3808
TELEFAX: (610) 454-3
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0
108 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-11170
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LENGTH: 622
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US-08-256-938-2
                                                                                                                                                                                                                                                                                                    US-09-984-186-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: C
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Gaps

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Sequence 3, Application US/08897956A
Patent No. 6423512
GENERAL INFORMATION:
APPLICANT: Mary Ellen Digan
APPLICANT: Philip Lake
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                                      RESULT 19
US-09-984-186-16
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Sequence 16, Application US/08797689
Patent No. 5876569
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Yellow, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Score 123; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                Length 787;
                                                                                                                             0; Indels
                                                                     100.0%; Score 123; DB 1; illarity 100.0%; Pred. No. 2.6e-11; Conservative 0; Mismatcher A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA

APPLICATION UNMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CIASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: 2792006-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (610) 454-3889
TELEPAX: (610) 454-3809
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERIFICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 DAHKSEVAHRFKDLGEENFKALVL 226
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                                                                                                                                                                       1 DAHKSEVAHRFKDLGEENFKALVL 24
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 787 amino acids
amino acid
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MOLECULE TYPE: protein
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-256-938-4
                                                                                Query Match
Best Local Similarity
Matches 24; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Macintosh
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-OCt-2001
CLASSIPTCATION - UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: R 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: P 92/01064
FILING DATE: 31-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 123; 5.6
Best Local Similarity 100.0%; Pred. No. 2.6
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-984-186-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
                                                                                             Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 DAHKSEVAHRFKDLGEENFKALVL 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 16, Application US/09984186 Patent No. 6686179 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 787 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relefax: (610) 454-3808
                                                                    APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                          CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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DANIEL C.
BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
RELATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DANIEL C.
BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
RELATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 88.6%; Score 109; DB 1; Length 583; all Similarity 83.3%; Pred. No. 3.3e-09; 20; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BROAD UR., ROBERT L.
REGISTRATION NUMBER: 18 757
REFERENCE/DOCKET NUMBER: 18 757
REFERENCE/DOCKET NUMBER: 18 757
REFERENCE/DOCKET NUMBER: 205-544-021
TELEPHONE: 205-544-025
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US-08-448-196A-7
Sequence 7, Application US/08448196A
PARENT No. 5780594
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
WUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSERS: NASA
STREET: MANSHALL SPACE FLIGHT CENTER
CITY: HUNTSYLLLE
STATE: ALABAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: MARSHALL SPACE FLIGHT CENTER CITY: HUNTSVILLE
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; Sequence 4, Application US/08448196A
; Patent No. 5780594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CARTER, DANIE
TITLE OF INVENTION: BIOLI
TITLE OF INVENTION: CONT
TITLE OF INVENTION: RELA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: ALABAMA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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83.3%; Pred. No. 3.3e-09;
tive 2; Mismatches 2; Indels
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Products and Method Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

PEPLICANT: Strand, Frederick T
TITLE OF INVENTION:
Denatured Bovine Serum Albumin Mil.
TITLE OF INVENTION: Denatured Bovine Serum Albumin Mil.
TITLE OF INVENTION: Products and Method Therefor
NUMBER OF SEQUENCES: 1
CORRESPONDERS Hand
STREET: P.O. Box 64321
CITY: Phoemix
STATE: Arizona
COUNTRY: USA
ZIP: 85082-4321
COMPUTRY: USA
ZIP: B6082-4321
COMPUTRY: IBM PC
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.1
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,638
FILING DATE: 10/12/93
CLASSIFICATION NUMBER: N/A
ATTORNEY ARBUT NUMBER: N/A
ATTORNEY ARBUT NUMBER: N/A
ATTORNEY ARBUT NUMBER: 19,497
REGISTRATION NUMBER: 19,497
REFERENCE/DOCKET NUMBER: TSEECOMMONICATION NUMBER: TELECOMMONICATION NUMBER: TSEECOMMONICATION NUMBER: TELECOMMONICATION NUMBER: TSEECOMMONICATION NUMBER: TSEECOMMONICATION NUMBER: TRELECOMMONICATION NUMBER: TOPE TOPE TRELECOMMONICATION NUMBER: TOPE TOPE TRELECOMMONICATION TRELECOMMONICATION TRELECOMMONICATION TRELECOMMONICATION TRELECOMMONICATION TRELECOMMONICATION TRELECOMMONICATION TRELECOMMONICATION TRELECOM
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100.0%; Score 123; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0;
APPLICANT: Hermann Gram
TITLE OF INVENTION: Fusion Polypeptides
FILE REFERENCE: 600-7244/CPA
CURRENT APPLICATION NUMBER: US/08/897,956A
CURRENT PILING DATE: 1997-07-21
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 DAHKSEVAHRFKDLGEENFKALVL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                    ), OTHER INFORMATION: Fusion polypeptide US-08-897-956A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DAHKSEVAHRFKDLGEENFKALVL 24
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                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (602) 947-2663
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single ; TOPOLOGY: linear US-08-134-638-1
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Best Local Similarity 83.3
Matches 20; Conservative
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DANIEL C.
BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR RELATED PROTEINS
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Pred. No. 9.18-08;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                    Length 583;
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ZIP: 35812
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAX-1995
CLASSIFICATION: 530
ATTONERY/AGENT INFORMATION:
NAME: BROAD JR.; ROBERT L.
REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 205-544-0021
TELEPHONE: 205-544-0021
TELEPHONE: 205-544-0025
                                                                                                                                                                                                                                                                Score 105; DB 1;
Pred. No. 1.4e-08;
2; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: NASA
STREET: MARSHALL SPACE FLIGHT CENTER
CITY: HUNTSVILLE
STATE: ALABAMA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DAHKSEVAHRFKDLGEENFKALVL 24
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Sequence 5, Application US/08448196A
Patent No. 5780594
GENERAL INFORMATION:
APPLICANT: CARTER, DANIEL C.
TITLE OF INVENTION: CONTAINING SPECTION:
TITLE OF INVENTION: RELATED PROTEIN:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: 205-544-000-1 TELEPAX: 205-544-000-1 S.
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 583 amino acids TYPE: amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0%;
Matches 18; Conservative
                                   , WOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-448-195A-6
                                                                                                                                                                                                                                                                       85.4%;
ilarity 79.2%;
Conservative
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Best Local Similarity
Matches 19; Conserva
                         TYPE: amino acid
TOPOLOGY: linear
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US-09-845-764A-1
LENGTH:
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Sequence 6, Application US/08448196A
Betent No. 5780594
GENERAL INFORMATION:
APPLICANT: CARTER, DANIEL C.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRACMENTS
TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR TITLE OF INVENTION: RELATED PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NAGA
STREET: MARSHALL SPACE FLIGHT CENTER
CITY: HUNTSVILLE
STATE: ALABAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 9.9e-09;
4; Mismatches 1; Indels
                                                                                                                                                                      OURENTING SYSTEM:
CURRENT APPLICATION DATA:
PELLON DATE:
PELLON DATE:
PELLON DATE:
PILNG DATE:
CLASSIFICATION:
NAME:
REGISTRATION:
NAME:
REGISTRATION NUMBER:
PELEPHONE:
TELEPHONE:
TOS-544-0021
TOPOLOGY:
TYPE:
MOMERTION TOS-544-0021
TYPE:
TYPE:
TYPE:
MOMERTION TYPE:
TOPOLOGY:
TO
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: Datentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/448,196A

FILING DATE: 23-MAY-1995

CLASSIFICATION: 53.0

ATTORNEY/AGENTION: ROBERT L.

NAME: BROAD JR., ROBERT L.

REGISTRATION NUMBER: 18,757
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 205-544-0021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DAHKSEVAHRFKDLGEENFKALVL 24
                                ZIP: 35812
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 79.2%;
Matches 19; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Patrick W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
APPLICANT: Chicago
STATE: Illinois
COUNTRY: USA
                          Query Match 56.9%; Score 70; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 0.0001; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.9%; Score 70; DB 1; I
100.0%; Pred. No. 0.0001;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: No. 5641669and, Greta E. REGISTATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 32205 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-483-232-1
; Sequence 1, Application US/08483232
; Patent No. 5656431
; GENERAL INPORMATION:
                                                                                                                                                                                                                                        Sequence 1, Application US/08318905
Patent No. 5641669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELBEAX: (312,
TELBEAX: (312,
TELBEAX: 25-3658
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                  1 FKDLGEENFKALVL 14
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                           RESULT 28
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Sequence 1, Application US/09845764A
Patent No. 6633080
GRNERAL INFORMATION:
APPLICAMT: Jackowaki, George
APPLICAMT: Jackowaki, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1521 DALTONS
FILE REFERENCE: 2132.037
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO : 1
SEQ ID NO : 1
LENGTH: 15
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Sequence 1, Application US/08470187;
Setent No. 5532152;
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine E.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Larry W.
TITLE OF INVENTION: Platelet-Activating Factor Acetyl;
TITLE OF INVENTION: Platelet-Activating Factor Acetyl;
TITLE OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun STREET: Chiscole Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                60.2%; Score 74; DB 4; Length 15; 100.0%; Pred. No. 2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60606
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/08/470,187
                                                                                                                                                                                                                                                                                                                                                            100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: NO. 552152and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31672
TELECOMMUNICATION INFORMATION:
TELEPRAN: (312) 474-6300
TELEFAX: 25.3658
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAHKSEVAHRFKDL 15
                                                                                                                                                                                                                                                                                                                                                                                                                             1 DAHKSEVAHRFKDL 14
                                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-08-470-187-1
                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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US-08-470-187-1
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APPLICANT: COUGEN, Lawrence S.
APPLICANT: Cougens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: To alker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 36
CORRESSED: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUWTRY: United States of America
ZIP: 6666-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: Darantin Palasae #10 Vargion #105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.9%; Score 70; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 0.0001; Matches 14; Conservative 0; Mismatches 0; Indels
                     MEDIUM TYPE FIREMY
COMPUTER: TAIDAY GISK
COMPOTER: TAIDAY GISK
COMPOTER: TAIDAY
APPLICATION NUMBER: US 08/18,905
FILNG DATE: C-CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/13,803
FILNG DATE: C-CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILNG DATE: C-CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5698401304
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LUMPGTH: 17 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PATCHTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,938A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 06-0CT-1994
PRIOR DATE: 06-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08485938A Patent No. 5847088 GENERAL INFORMATION:
       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 FKDLGEENFKALVL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FKDLGEENFKALVL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-08-483-140-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-08-485-938A-1
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APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hail
APPLICANT: Tjoelker, Larry W.
APPLICANT: Gray Larry W.
APPLI
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                                                                                                                                                                                                                                                                                                                                                                                                     CITKELI: 0.3 UD SEGIES TOWER, 2.3.3 SOUTH WACKET DITUE
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 60.60-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
ORPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAMME: NO. 5656413and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37,302
REFERENCE/DOCKET NUMBER: 37,300
TELLEPHONE: (312) 474-6300
TELLEPHONE: (312) 474-6300
TELLEPHONE: (312) 474-6300
TELLEPHORE: 25-3658
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FKDLGEENFKALVL 14
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Best Local Similarity 100.
Marches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide US-08-483-232-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60606
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Berhardt, Christine D.
APPLICANT: Toelker, W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Graphydrolase
NUMBER OP SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                 Query Match 56.9%; Score 70; DB 2; Length 17; Best Local Similarity 100.0%; Pred. No. 0.0001; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTERET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111hnois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER: Elbabale Form:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,474
FILING DATE:
CLASSIFICATION TAR:
APPLICATION NUMBER: US/09/328,432
FILING DATE:
CLASSIFICATION NUMBER: US 08/483,232
FILING DATE:
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 06-OCT-1994
PRICK APPLICATION NUMBER: US 08/133,803
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, 1-1981
NEFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09328474 Patent No. 6045794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 anino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FKDLGEENFKALVL 14
                                                                                                                                                                                                                                                                                                                                                                                               11 FKDLGEENFKALVL 24
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 17 amino acids
                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-09-328-474-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
US-09-328-474-1
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Sequence 1, Application US/08910041

Fatent No. 5977308

Fatent No. 5977308

FAPLICANT: Coueens, Lawrence S.

APPLICANT: Bebrhardt, Christine D.

APPLICANT: Bebrhardt, Christine D.

APPLICANT: Le Trong, Hai

APPLICANT: Wilder, Cheryl L.

TITLE OF INVENTION: Platelet-Activating Factor

TITLE OF INVENTION: Acctylhydrolase

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STREET: Giology disk

COUNTRY: United States of America

ZIP: 66606-6402

COMPUTER: IBM C Compatible

COMPUTER: IBM C Compatible

COMPUTER: IBM PC Compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION DATA:

PLIANG DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 2; Length 17; Pred. No. 0.0001; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.9%; Score 70; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 14; Conservative 0; Mismatches
                     FILING DATE: 06-0CT-1993
ATTORNEY AGENT INFORMATION:
NAME: NO. 5847088and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32792
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-648
TELEFAX: (312) 474-648
TELEFAX: 132, 474-648
TELEFAX: 132, 674-686
SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 17 amino acide
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERNICE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION NUMBER: US 08/33,803
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
         APPLICATION NUMBER: US 08/133,803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (312) 474-6300
(312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 FKDLGEENFKALVL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FKDLGEENFKALVL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-485-938A-1
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Sequence 1, Application US/09010715; Patent No. 6146625; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
       US-09-010-715-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.9%; Score 70; DB 3; Length 17; 100.0%; Pred. No. 0.0001; ive 0; Mismatches 0; Indels
         Score 70; DB 3; Length 17;
Pred. No. 0.0001;
                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111nois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: PC-DOS/MS-DOS COMPUTER: IBM PC COMPATIBLE OF SOUTH OF SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/100,546
                                                                                                                                                                                                          APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Lary W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor TITLE OF INVENTION: Acetylhydrolase NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS:
ADDRESSEE: Marsh.
56.9%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLING DATE:
APPLICATION NUMBER: US 08/318,905
FLING DATE: 06-0CT-1994
PRILING DATE: 06-0CT-1994
PRILING DATE: 06-0CT-1993
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6099336and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37866/32793
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6448
INPORMATION FOR SEQ ID NO: 1:
SEGURACE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FKDLGEENFKALVL 14
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                                                                                                               1 FKDLGEENFKALVL 14
                                                                                     11 FKDLGEENFKALVL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 17 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 14; Conservative
                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-100-546-1
                                                                                                                                                                               RESULT 34
US-09-100-546-1
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RESULT 35

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APPLICANT: Couesns, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Erary, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Darry W.
APPLICANT: Tjoelker, Darry W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                       STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: PILING DATE: PATENT DATA: US/09/010,715 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Cousens, Christine D.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.9%; Score 70; DB 3; I
100.0%; Pred. No. 0.0001;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
FILING DATE: 06-OCT-1993
ATTOKNEY/AGENT INFORMATION:
NAME: No. 6146625and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 104-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-577-758-1; Sequence 1, Application US/09577758; Patent No. 6203790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 FKDLGEENFKALVL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3658
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.3%; Score 68; DB 2; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCE.

CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
ADDRESSEE: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUMRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,198
FILING DATE: 17 FEB 1998
CLASSIFICATION NUMBER: 08/803,364
FILING DATE: 20 FEB 1997
CLASSIFICATION NUMBER: A-6988
FILING DATE: 20 FEB 1997
CLASSIFICATION INFORMATION:
MAME: KIT, GOTGON
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: 3-7060
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 13:
CDATEMATICAL CORP.
TELEFRAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL APLICANT: FASANO, Alessio
APPLICANT: FASANO, Alessio
TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SKAS
                                                                                                                                                                                                           A-6888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-024-198-13
; Sequence 13, Application US/09024198
; Patent No. 5912323
                        FILING DATE: 20 FEB 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KIT, GOTGON
REGISTRATION NUMBER: 30,764
REPERROKE/DOCKET NUMBER: A-68E
TELEPHONE: (202) 293-7860
INFORMATION: CALLANDER C
APPLICATION NUMBER: 08/
FILING DATE: 20 FEB 1997
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LENGTH: 13 amino acids
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NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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MOLECULE TYPE:
HYPOTHETICAL: N
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                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Marehall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.9%; Score 70; DB 3; Length 17; 100.0%; Pred. No. 0.0001; tive 0; Mismatches 0; Indels
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Sequence 7, Application US/08803364

Patent No. 5864014

GENERAL INFORMATION:

APPLICANT: FASANO, Alessio

ITILE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W., Suite 800

CITY: Washington, D.C.

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20037
                                                                                                                                        CITY: Cnlcago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
COUNTRR READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,758
FLING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/010,715
FLING DATE:
APPLICATION NUMBER: 09/010,715
FILING DATE: 06-OCT-193
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 35,302
FLING DATE: 35,302
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6448
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TTENGTH: 17 amino acids
TTENGTH: 17 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/803,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 FKDLGEENFKALVL 24
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Matches 14; Conservative
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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CORRESPONDENCE ADDRESS:
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                        Gaps
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                                                                                                                                                                                                   Sequence 13, Application US/09186409

Patent No. 5948629

GENERAL INFORMATION:
APPLICANT: FASANO, Alessio
TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: SUGHRUE, MON, ZINN, MACPEAK & SEAS
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
                        0; Indels
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Patent No. 5864014
GENERAL INFORMATION:
APPLICANT: FASANO, Alessio
TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/186,409
FILING DATE: 5 NOV 1998
CLASSIFICATION:
  100.0%; Pred. No. 0.00015;
                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/024,198
FILING DATE: 17 FEB 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,364
FILING DATE: 20 FEB 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERRENCE/DOCKET WUMBER: A-7306
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ ID NO: 13:
LENGTH: 13 amino acide
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Best Local Similarity 100.
Matches 13; Conservative
                                                                 2 AHKSEVAHRFKDL 14
                                                                                         Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO
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GY: linear
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US-08-803-364-1
    Best Local
Matches 1
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CURRENCUENCE AUDAREASE

CURRENT 2100 Pennsylvania Avenue, N.W., Suite 800

CITY: Weathington, D.C.

COUNTRY: 0.C.

COUNTRY: 0.C.

COMPUTER: EMP PC compatible

COMPUTER: TRANDALE FORM:

MEDILOTION TYPE: TOOPP disk

COMPUTER: HEM PC compatible

CLASSIFICATION NUMBER: 08/

FILING DATE: 20 FEB 1997

CLASSIFICATION NUMBER: 09/

FILING DATE: 20 FEB 1997

CLASSIFICATION NUMBER: 08/

FILING DATE: 08/

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AAM84996
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Abu08846 Serum alb
Abu75592 Human ser
Abu09223 Serum alb
Abu09223 Serum alb
Aa01632 Human pol
Aa011632 Human pol
Aa011632 Human pol
Aa017048 Human ser
Abu10022 Human ser
Abu10022 Human ser
Abu10022 Human alb
Aa045984 Alpha-MSH
Aa046984 Alpha-MSH
Aa016986 Alpha-MSH
Aa016986 Alpha-MSH
Aa016987 Alpha-MSH
Aa016988 Alpha-MSH
Aa016989 Alpha-MSH
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                                                          August 19, 2005, 10:48:50 ; Search time 163 Seconds (without alignments) 56.946 Million cell updates/sec
                                                                                                                                                                          2105692
         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                       2105692 seqs, 386760381 residues
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                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match ]
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	Determining proteomic basis e.g. basis for diagnosing existence of predicting development and/or progression of abnormal physiological conditions based upon the presence of proteomic materials. Disclosure; Page 22; 25pp; English.	sclos isolisol char char for norm
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AA016988 AA016989

ABU10026 AAU29581

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Query Match
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Entered 24; Conservative
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MARSHALL J.
YANTHA J.
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Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                     ABU08847;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new biopolymer marker useful in indicating a particular disease state particularly insulin resistance.
the presence of physiological condition specific sequences. The peptide presented is a biomarker from serum albumin and is associated with
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                               Human; serum albumin; biopolymer marker; SELDI;
Surface Enhanced Laser Desorption Ionization mass spectrometry;
time-of-flight detection procedure; complement system disease;
syndrome X; insulin resistance; hyperinsulinaemia.
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                                                                                     Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Specifically claimed in claim 1"
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                                                                                     100.0%; Score 123; DB 6; 100.0%; Pred. No. 1.6e-12;
                                                                                                                                                                                                                                                                                                                                    Human serum albumin biopolymer marker peptide.
                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Optionally absent"
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                                                                                                                                                               DAHKSEVAHRFKDLGEENFKALVL 25
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Best Local Similarity
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                                 insulin resistance
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VREES T.
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                                                          Sequence 26 AA;
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indicating insulin resistance

Sequence 26 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteomic; human; physiological condition; analyte; biopolymer;
biomarker; serum albumin; insulin resistance.
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                        Score 123; DB 6;
Pred. No. 1.6e-12;
100.0%; Scc.
100.0%; Pred. No. 100.0%; O; Mismatches
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(first entry)

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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                               Human polypeptide SEQ ID NO 16534.
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18-MAY-2000; 2000US-00577409
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a serum albumin biopolymer marker having a molecular weight of 2937 daltons which indicates at least one particular disease state. The bioploymer marker is useful for indicating at least one particular disease state. The bioploymer marker is useful for indicating at least one particular disease state. e.g. insulin resistance. Also for diseases associated with the complement system and syndrome X such as obesity, hyperinsulinaemia, lipsemia, glucose intolerance, blood coagulation abnormalities, hyperuricaemia, albuminuria, kidney failure, stroke, hypertension, diabetes and heart failure. The biopolymer marker enables a diagnostician to gain the ability to characterise either the presence or absence of the disease state relative to recognition of the presence and/or the absence of the biopolymer. The present sequence represents the amino acid sequence of the serum albumin insulin resistance disease
                                                                                                                                                                                                                                      Human; insulin resistance; serum albumin; biopolymer marker; lipaemia; complement system disease; syndrome X; obesity; hyperinsulinaemia; glucose intolerance; blood coagulation abnormality; hyperuricaemia; albuminuria; kidney failure; stroke; hypertension; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serum albumin biopolymer marker having specific molecular weight
indicates at least one particular disease state.
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                                                                                                                                                                                             Serum albumin insulin resistance disease specific marker.
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100.0%; Pred. No. 1.7e-12;
cive 0; Mismatches 0;
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                                                  ABU09223 standard; peptide; 28 AA
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MARSHALL J.
YANTHA J.
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                                                                                                                                                                                                                                                                                                                                           heart failure
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                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                                                                                                                                                                                                                                                                               directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Claim 20; SEQ ID NO 16534; 1399pp + Sequence Listing; English
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100.0%; Pred. No. 8.6e-12;
ative 0; Mismatches 0;
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Matches

AAO02642 standard; protein; 116 AA

RESULT 5. AAO02642 ID AAO(

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Homo sapiens.
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                                                                                                                                                                                                              Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                            The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence encoded by recombinant DNA molecule pKT218(HSA/33-1 (Eg1II-EcoRI)-HSA/17-3(Eg1II-EcoRI)) human proserum albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burn therapy, blood, protein, nitrogen fixation, food additive, kernicterus therapy.
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                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 25524; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 123; DB 4; Length 119; 100.0%; Pred. No. 8.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
nervous system disorders; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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/label= residues 319-351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP30004 standard; protein; 133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l. .26
/label= signal
                                                                                  26-FEB-2001; 2001WO-US004927
                                                                                                      28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                          Fang YT, Liu C, Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Conservative
                                                                                                                                                                               WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                          N-PSDB; AAI91563
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 119 AA;
                                         WO200164835-A2
                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-1992
                                                             07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP30004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Prodn. of human serum albumin-like polypeptide(s) - from host transformed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 123; DB 1; Length 133; 100.0%; Pred. No. 1e-11; ive 0; Mismatches 0; Indels (
. .124
abel= residues 368-399
                                                                                    /label= residues 572-580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 DAHKSEVAHRFKDLGEENFKALVL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DAHKSEVAHRFKDLGEENFKALVL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU29875 standard; protein; 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with recombinant DNA molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 4; 42pp; English.
                                                                                                                                                                                                                                                                                                                               81US-00330912.
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                                                                                                                                                                                                                                                                   81US-00330912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2000; 2000US-00552929
26-JAN-2001; 2001US-00770160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1983-796520/43.
N-PSDB; AAN30009.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gilbert W, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 133 AA;
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Novel
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                                                                          The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated (with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent (for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins care useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell condition are also useful for producing immune suppression and/or sufform rerve tissue growth or regeneration; immune suppression and/or sufform estimation; as anti-inflammatory agents; and in bone, cartilage, tendon stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

ANUZ9510-AAU331304 represent the anino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                            ö
                     Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive; antiinflammatory; antiheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antipsoriatic; antidabetic; ophthalmological; heuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.
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                                                                                                                                                                                                                                                                                                                                     100.0%; Score 123; DB 4; Length 192;
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                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                  1.5e-11;
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human serum albumin (1-195) SEQ ID NO: 56
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                                                                                                                                                                                                                                                                                                                                                                                                      DAHKSEVAHRPKDLGEENFKALVL 76
                                                                                                                                                                                                                                                                                                                                                                                      1 DAHKSEVAHRFKDLGEENFKALVL 24
                                                           Claim 20; Page 206; 765pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA017048 standard; protein; 195 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0218381P.
2000US-0226382P.
2000US-0238380P.
2000US-0258764P.
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                                                                                                                                                                                                                                                                                                                                                  100.08;
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                                                                                                                                                                                                                                                                                                                                                             24; Conservative
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WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYCO-) ZYCOS INC
                                                                                                                                                                                                                                                                                                             Sequence 192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200206316-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA017048;
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                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                        The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an albha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a protein described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating immune responses in a mammal with a bladder disorder e.g. bladder cancer, by administering nucleic acids comprising un-methylated CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides to the mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a method of modulating an immune response in a mammal, comprising identifying a mammal that has or is at risk for having a bladder disorder, and administering: (a) an isolated nucleic acid (NI) comprising an un-methylated CpG sequence to the mammal; (b) an isolated nucleic acid (N2) comprising sequence encoding alpha-MSH to the mammal;
nucleic acid encoding fusion protein comprising alpha-melanocyte lating hormone concatamer or its analog, for treating inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bladder disorder; cytostatic; antiinflammatory; immune response; un-methylated CpG sequence; alpha-MSH; melanocortin receptor; bladder cancer; tumour; interstitial cystitis; inflammation; alpha-MSH concatamer; melanocyte stimulating hormone; human; serum albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 123; DB 5;
Pred. No. 1.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DAHKSEVAHRFKDLGEENFKALVL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU10022 standard; protein; 195 AA.
                                                                                                                                          Example 2; Page 46; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                        or autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-447327/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002193332-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-2003
                                        stimulating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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the process for producing human serum albumin in the yeast host cell, especially in secretory mode

Sequence 204 AA;

SXSS

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method is useful for modulating immune response in a mammal. The method is useful for modulating immune response in a mammal having a bladder disorder, where administration of (NI) results in an ameloration of one or more symptoms of the disorder. Preferably, the method is useful for modulating immune response in a mammal having bladder cancer (where administration of (NI) results in a decrease in tumour size or activity), or for modulating immune response in a mammal having interstitial cystitis (where administration of (NI) results in a modulation of the immune response from Th2 response to a Th1 response). The method is also useful for modulating immune response to a Th1 response). The method is also that is characterised by inflammation which is associated with symptoms of interstitial cystitis or associated with a disruption of the integrity of interstitial cystitis or associated with a disruption of the integrity albumin residues lining This is the amino acid sequence of human serum albumin residues l-195 that can be used in the creation of melanocyte etimulating hormone (alpha-MSH) concatamers resulting in secretion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The method relates to a method of recombinantly producing human serum albumin (HSA) in yeast by altering the coding sequence of HSA to comprise a yeast codon bias. The complete HSA gene (AAA10091) was generated as three synthetic fragments (AAA10092-A10094) joined by recombinant DNA technology. Each HSA fragment was synthesised from overlapping oligonucleotide fragments that were extended. This sequence represents the sequence of the HSA fragment HSA-1 encoded by the human gene with a yeast codon bias. The invention also covers a recombinant expression vector, yeast host cells carrying the recombinant expression vector and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Process for preparing recombined human serum albumin comprising yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant; human serum albumin; HSA; yeast codon bias; host cell; overlapping oligonucleotide; expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                            Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast codon-biased recombinant HSA protein fragment HSA-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biased sex codons - uses a recombinant DNA technique.
                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 123; DB 7; 100.0%; Pred. No. 1.6e-11;
                                                                                                                                                                                                                                                                                                              fusion protein when expressed in mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAHKSEVAHRFKDLGEENFKALVL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HAIJ-) HAIJI BIOENGINEERING CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY83947 standard; protein; 204 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98CN-00102506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA10092
                                                                                                                                                                                                                                                                                                                                                      Sequence 195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lu D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY83947;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or stimulation; as anti-inflammatory agents; and in treatment of leading. AAU29510-AAU33304 represent the amino acid sequences of novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                          Indels
                          Score 123; DB 3;
Pred. No. 1.6e-11;
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100.0%; Pred. No. 1.7e-11;
ive 0; Mismatches 0;
100.0%; Scc...
100.0%; Pred. No. ...
                                                                                                                                                                                               8 DAHKSEVAHRFKDLGEENFKALVL 31
                                                                                                                                                          1 DAHKSEVAHRFKDLGEENFKALVL 24
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                                                                                                                                                                                                                                                                                                                                                                                     AAU29874 standard; protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted protein #365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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Best Local Similarity 100.
Matches 24; Conservative
                                                                                              24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-611725/70.
                                 Query Match
Best Local Similarity
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The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concaremer. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatorid arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a protein described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory
                                                                                                                                                                             Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive, antiinflammatory, antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antipsoriatic; antidiabetic; ophthalmological; neuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Etemad-Moghadam B,
                                                                                                                                          Alpha-MSH construct protein fragment SEQ ID NO: 59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DAHKSEVAHRFKDLGEENFKALVL 24
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                   AA016984 standard; protein; 241 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-2000; 2000US-0218381P.
18-AUG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-0238380P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUL-2001; 2001WO-US022263.
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                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-195801/25
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                                                                                                                                                                                                                                                                                                                                                                                               WO200206316-A2.
                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                     29-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU10025;
                                                              AA016984;
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual suffering from, or a trisk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatory disorder or autoimmune disorder, including rheumatoid arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabeces, luque, uveitis and coeliac disease. The present sequence is a peptide described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                   Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive; antiinflammatory, antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antipsoriatic; antidiabetic; ophthalmological; neuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Etemad-Moghadam B,
                                                                                                                                                                                                                                                                                              Human albumin-thrombin-alpha-MSH SEQ ID NO: 82.
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                                                                                                                                                                       AAO17051 standard; protein; 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aziz N,
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18-MG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-023880P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
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                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-195801/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                       29-MAY-2002
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alpha-melanocyte stimulating hormone, rheumatoid arthritis, sephis; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive; antinflammatory; antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antipsoriatic; antidiabetic; ophthalmological; neuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.

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The invention describes a method of modulating an immune response in a mammal, comprising identifying a mammal that has or is at risk for having a bladder disorder, and administering: (a) an isolated nucleic acid (NI) comprising an un-methylated CyG sequence to the mammal; (D) an isolated nucleic acid (NZ) comprising sequence encoding alpha-MSH to the mammal: The nucleic acid (NZ) comprising sequence encoding alpha-MSH to the mammal. The method is useful for modulating immune response in a mammal having a bladder disorder, where administration of (NI) results in an analloration of one or more symptoms of the disorder. Preferably, the method is useful for modulating immune response in a mammal having bladder cancer (where administration of (NI) results in a modulation of the immune response in a mammal having interstitial where administration of (NI) results in a modulation of the immune response in a mammal having bladder disorder that is characterised by inflammation which is associated with symptoms of interstitial cystitis or associated with a disruption of the integrity of the bladder lining. This is the amino acid sequence of a human serum melanocyte stimulating hormone (alpha-MSH) concatamer useful in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating immune responses in a mammal with a bladder disorder e.g. bladder cancer, by administering nucleic acids comprising un-methylated CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                 Bladder disorder; cytostatic; antiinflammatory; immune response; un-methylated CpG sequence; alpha-MSH; melanocortin receptor; bladder cancer; tumour; interstitial cystitis; inflammation; alpha-MSH concatamer; melanocyte stimulating hormone; human; serum albumin; fusion protein; H9.
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Alpha-MSH/Serum albumin fusion protein H9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of bladder disorders
                                                                                                                                                                                                                                                                                               12-FEB-2002; 2002US-00074956.
                                                                                                                                                                                                                                                                                                                                      12-FEB-2001; 2001US-0268175P
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                                                                                                                                                                                                                                                                                                                                                                              (HEDL/) HEDLEY M L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                 US2002193332-A1.
                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                          19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mammal.
                                                                                                                                                                             Synthetic.
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Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.

Disclosure; Page 5; 89pp; English.

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Etemad-Moghadam B,

Chen H,

Aziz N,

Hedley ML, Urban R, WPI; 2002-195801/25.

ZYCO-) ZYCOS INC.

18-AUG-2000; 2000US-0226382P. 06-OCT-2000; 2000US-0238380P. 29-DEC-2000; 2000US-0258764P. 14-JUN-2001; 2001US-0298317P.

16-JUL-2001; 2001WO-US022263 14-JUL-2000; 2000US-0218381P.

WO200206316-A2 Unidentified

24-JAN-2002.

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The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a protein described in the exemplification of the
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0; Mismatches 0;
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Alpha-MSH construct protein fragment SEQ ID NO: 70.

(first entry)

29-MAY-2002

AA016985;

AAO16985 ID AAO XX AC AAO XX DT 29-

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AAO16985 standard; protein; 242

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                    Chen H,
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    diabetes; uveitis; coeliac disease.
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18-AUG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-0238880P.
29-DBC-2000; 2000US-0258764P.
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                                                                                                                                                                                                                                                                                                                                                                                    Urban R,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            (ZYCO-) ZYCOS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 244 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma; cirrhosis; dermatitis; psoriasis; inflammatory bowel disease; immunosuppressive; antiinflammatory, antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antipsoriatic; antidabetic; ophthalmological; neuroprotective; multiple sclerosis; diabetes; uveitis; coeliac disease.
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Pred. No. 2e-11;
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                                                 2000US-0218381P.
2000US-0226382P.
2000US-0238380P.
2000US-0258764P.
2001US-0298317P.
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100.0%;
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18-AUG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-0238380P.
29-DEC-2000; 2000US-0258764P.
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16-JUL-2001; 2001WO-US022263.
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Best Local Similarity luv..
Local 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               or autoimmune disorders.
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                                                                                                                                                                                                                       (ZYCO-) ZYCOS INC.
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                                                                                 18-AUG-2000;
06-OCT-2000;
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                                                       14-JUL-2000;
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                                                                                                                                                    The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual suffering from, or a risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatory arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a protein described in the exemplification of the
                                                                                     Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
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                                           Yin P;
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                                           Etemad-Moghadam B,
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                                                                                                                                Disclosure, Page 5, 89pp, English.
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                                           Aziz N,
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18-MG-2000; 2000US-0226382P.
06-OCT-2000; 2000US-023880P.
29-DEC-2000; 2000US-0258764P.
14-JUN-2001; 2001US-0298317P.
 14-JUN-2001; 2001US-0298317P
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                                          Urban R,
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                     (ZYCO-) ZYCOS INC
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                                          Hedley ML,
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The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uvaitis and coaliac disease. The present sequence is a protein described in the exemplification of the
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Novel nucleic acid encoding fusion protein comprising alpha-melanocyte stimulating hormone concatamer or its analog, for treating inflammatory or autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 123; DB 5; 100.0%; Pred. No. 2.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-MSH/Serum albumin fusion protein H4.
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                                                                                                                                                   Example 2; Page 5; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2002193332-A1.
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cc nucleic acid (N2) comprising sequence encoding alpha-MSH to the mammal; cc or (c) a peptide that binds to a melanocortin receptor to the mammal. The method is useful for modulating immune response in a mammal having a bladder disorder, where administration of (N1) results in an amelioration of one or more symptoms of the disorder. Preferably, the method is useful for modulating immune response in a mammal having bladder cancer (where administration of (N1) results in a decrease in tumour size or activity), or for modulating immune response in a mammal having interstitial cystitis (where administration of (N1) results in a modulation of the constitution of the immune response to a Th1 response). The method is a sloot useful for modulating immune response in a mammal having bladder disorder that is characterised by inflammation which is associated with symptoms of interstitial cystitis or associated with a disruption of the integrity of the bladder lining. This is the amino acid sequence of a human serum melannocyte stimulating hormone (alpha-MSH) concatamer useful in the reatment of bladder disorders 8566666666666666668566888

Sequence 268 AA;

Gaps ö 100.0%; Score 123; DB 7; Length 268; 100.0%; Pred. No. 2.2e-11; ive 0; Mismatches 0; Indels ( Pred. No. 2.2 0; Mismatches 1 DAHKSEVAHRFKDLGEENFKALVL 24 24; Conservative Query Match Best Local Similarity Matches 셤 ઠે

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AAU29581 standard; protein; 289 AA

(first entry) 18-DEC-2001 AAU29581;

Novel human secreted protein #72.

Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration, immune suppression, immune stimulation, anti-inflammatory, leukaemia.

Homo sapiens.

WO200179449-A2

25-OCT-2001.

16-APR-2001; 2001WO-US008656

18-APR-2000; 2000US-00552929. 26-JAN-2001; 2001US-00770160.

(HYSE-) HYSEQ INC.

Drmanac RT; Liu C, rang YT,

WPI; 2001-611725/70.

Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.

Claim 20; Page 168; 765pp; English.

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered 

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continuous tenerates to the polypeptides are useful for determining the presence of or predisposition to a disease associated determining the presence of or predisposition to a disease associated determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying a therapeutic agent expressing the proteins are useful for identifying a therapeutic agent or physiological interactions of the polypeptide or vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell or and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of lengan secreted proteins of the invention
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to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or atministant of setministation; as anti-inflammatory agents; and in treatment of leukaemias. AAU20510-AAU33104 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding a range of human polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, vaccination; gene therapy, nutritional supplement, stem cell proliferation; haematopoiesis, nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                 Length 289;
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                                                                                                                                                                                                               Score 123; DB 4;
Pred. No. 2.4e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAU29575 standard; protein; 289 AA.
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                                                                                                                                                                                                                 100.0%;
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26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                               Local Similarity 100.
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                                                                                                                                                                               Sequence 289 AA;
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N-terminal fragment of human serum albumin used as plasma expander, or as
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                                                                                                                                                                            New N-terminal fragments of human serum albumin - esp. useful as blood plasma expanders.
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                     Senior PJ;
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                                                                                                                                    Hinchliffe E, Geisow MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Geisow MJ,
                                                                                                                                                                                                                                                                                                                                                                                  1 DAHKSEVAHRFKDLGEENFKALVL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP90389 standard; protein; 388 AA.
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                                                                                                               (DELZ ) DELTA BIOTECHNOLOGY LTD
                                                                                                                                                                                                                    Claim 2; Page 9; 20pp; English.
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                                                                  88EP-00310000.
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Homo sapiens; (Human)
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                                                                                                                                                           WPI; 1989-186464/26.
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25-MAR-2003
01-NOV-1989
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                                                                                         30-OCT-1987;
                                                                                                                                     Ballance DJ,
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                                                                  25-OCT-1988;
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                     EP322094-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence corresponds to amino acids 1 to 303 of mature human serum albumin. The fragment lacking the C-terminal sequence can form part of a fusion protein, for example with drugs. (This sequence is taken from the full-length HSA sequence in EP-330451). See also AAR14179
                                                        Gaps
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                                 Length 289;
                                                        Indels
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                                100.0%; Score 123; DB 4;
100.0%; Pred. No. 2.4e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                 C-terminal fragment.
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                                                                               1 DAHKSEVAHRFKDLGEENFKALVL 24
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                                                                                                                                                                                                                                                                                                                                                 89JP-00344701.
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                                                                                                                                                                                                                                 Human serum albumin lacking
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Best Local Similarity 100..
Loca 24; Conservative
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                                            Local Similarity 100.
Les 24; Conservative
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            Sequence 289 AA;
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25-MAR-2003
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                                 Query Match
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                                                        Matches
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11D AAP9
XX AC AAP6
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N-terminal portion of human serum albumin. Used to make new N-terminal fragments which are used as plasma expanders, or as substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                     New N-terminal fragments of human serum albumin - esp. useful as blood
plasma expanders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemla.
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                                                                        N-terminal portion of human serum albumin; plasma expanders.
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                                             N-terminal human serum albumin.
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26-JAN-2001; 2001US-00770160.
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                (first entry)
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Best Local Similarity 100.1
Matches 24; Conservative
(revised)
                                                                                                          Homo sapiens; (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 390 AA;
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25-MAR-2003
01-NOV-1989
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 substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New N-terminal fragments of human serum albumin - esp. useful as blood
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                                                                                               Length 388;
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100.0%; Score 123; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0;
                                                                                          Query Match
100.0%; Score 123; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0;
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                                                                  Sequence 388 AA;
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25-MAR-2003
01-NOV-1989
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RESULT 28

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                                                                          The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells of expressing the proteins are useful for identifying at the proteins are useful for identifying at the protein or public as a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and calls genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoissis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or atmunation, as anti-inflammatory agents; and in treatment of leukaemias.

AANT9510-AANJ3304 represent the amino acid sequences of novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human serum albumin; mature protein; new polypeptides; plasma expanders.
                   Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP90392 standard; protein; 407 AA
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                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                              Sequence 401 AA;
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01-NOV-1989
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comprising a hyperglycosylated granulocyte-colony stimulating factor (G-camprising a hyperglycosylated granulocyte-colony stimulating factor (G-camporising a hyperglycosylated granulocyte-colony stimulating factor (G-camporising a hyperglycosylated should human albumin, or the Fc portion of an immunoglobulin, or immunoglobulin, an analogue of the Fc portion of an immunoglobulin, or fragments of the Fc portion of an immunoglobulin. Also described: (1) a certagments of the Fc portion of an immunoglobulin. Also described: (1) a composition of the product of the expression in a host cell of an exogenous DNA sequence encoding (I); (2) an isolated comprising: (a) polymucleotides encoding (I); or comprising 1044 base pairs (see ADD131996 to ADD12010), fused to the DNA cenceding a protein (i.e. human albumin, human albumin analogue or comprising the administration of (I); (4) pharmaceutical formulations comprising the administration of (I); (4) pharmaceutical formulations adapted for the treatment of patients with insufficient neutrophil levels comprising any of (I); (5) a vector comprising the polymucleotide of (2); (6) host cells comprising the vector of (5), or expressing at least one thereologous protein; and (7) producing (I). (I) has immunostimulant activity, and can be used in protein therapy. (I) can be used for
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-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New heterologous fusion proteins with granulocyte-colony stimulating factor activity, useful for increasing neutrophil levels and treating patients with low circulating neutrophils, such as after chemotherapy or
                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyperglycosylated granulocyte-colony stimulating factor; G-CSF; human albumin; human albumin analogue; immunoglobulin; Fc; immunostimulant; protein therapy; neutrophil level; insufficient circulating neutrophil level;
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0
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Pred. No. 3.6e-11;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               1 DAHKSEVAHRFKDLGEENFKALVL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heterologous fusion protein;
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                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                   Sequence 407 AA;
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta KA, Blanchard JL, Pioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, encodernine disorder, neurological disorders, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
 are particularly useful in
medicaments for the treatment of patients with insufficient circulating medicaments for the treatment of patients with insufficient circulating treatments, or for the manufacture of a medicament for the treatment of patients with insufficient circulating neutrophil levels. The fusion protein is particularly useful for treating conditions treatable by stimulation of dirculating neutrophils, such as after chemocherapy regimens or in chronic congenital neutropenia. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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                                                                                                                                                                                                              100.0%; Score 123; DB 7; Length 500; 100.0%; Pred. No. 4.5e-11;
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2002US-0410260P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                              Sequence 500 AA;
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12-SEP-2002;
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Best Local S
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated determining the presence of or predisposition to a disease associated determining the presence of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent or physiological interactions of the polypeptide. Vectors comprising the complete acids encoding the polypeptides and cells genetically engineered nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins of an untritional supplements. They may be used to increase stem cell confirmation; to regulate haematopoiesis; and in bone, cartilage, tendon cell and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU32510-AAU33104 represent the amino acid sequences of novel human
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molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline some therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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stem cell proliferation, haematopoiesis, nerve tissue regeneration;
immune suppression, immune stimulation, anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                        AAU29877 standard; protein; 550 AA
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26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                            Sequence 544 AA;
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                                                                                                                                                                                               Query Match
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AAU29877
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Gaps

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Indels

100.0%; Score 123; DB 8; 100.0%; Pred. No. 5.3e-11; ive 0; Mismatches 0;

24; Conservative

Matches

Query Match Best Local Similarity

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ABM84996 standard; protein; 573 AA

Length 571;

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A purint cleotide of the invention may have a use in gene therapp. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine cutoimmune/inflammatory disorder, developmental disorders, or autoimmune/inflammatory disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp concluse may also be used in genetic mapping, in identifying individuals molecules may also be used in genetic mapping, in identifying individuals comparphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the gene therapy. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Pensear IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Ku Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletzer
Patury S, Shi X, Suarez CJ;
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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                                      Length 550;
                                                                                                                                                                                                                                                                                                                                                                      Human diagnostic and therapeutic pprotein SEQ ID NO:5246.
                                                                          Indels
                                    100.0%; Score 123; DB 4; 100.0%; Pred. No. 5.1e-11;
                                                                          0; Mismatches
                                                                                                                 1 DAHKSEVAHRFKDLGEENFKALVL 24
                                                                                                                                       DAHKSEVAHRFKDLGEENFKALVL 50
                                                                                                                                                                                                                                                    ABM84997 standard; protein; 571 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2002; 2002US-0410259P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2003; 2003WO-US028227
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                          Conservative
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                                                    Local Similarity
les 24; Conserv
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  Sequence 550 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2004.
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                                                                                                                                                                                                                                                                                           ABM84997;
                                      Query Match
                                                                            Matches
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L2-SEP-2003; 2003WO-US028227. 12-SEP-2002; 2002US-0410259P. 12-SEP-2002; 2002US-0410260P

WO2004023973-A2.

25-MAR-2004.

Homo sapiens.

(INCY-) INCYTE CORP.

Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolaki MT, Altus CM, Pittes SJ, Blder LV;
Mooney EM, Delegeane AM, Bensear IS, Banville SC, Reddy TP;
Stevens RA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

Suarez CJ;

Shi X,

Patury S,

WPI; 2004-329368/30. N-PSDB; ACN43648.

gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

Human diagnostic and therapeutic pprotein SEQ ID NO:5245.

(first entry)

18-NOV-2004

ABM84996;

New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

in gene mapping

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnost a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide collar was molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a ditup protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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Sequence 573 AA;

Sequence 571 AA;

5.3e-11;

Pred. No.

100.08;

Local

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Pensear IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletzel
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                         gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                            Gaps
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 Length 573;
                         Indels
                                                                                                                                                                                                                                  Human diagnostic and therapeutic pprotein SEQ ID NO:5244.
100.0%; Score 123; DB 8; I
100.0%; Pred. No. 5.3e-11;
ive 0; Mismatches 0;
                                                                         1 DAHKSEVAHRFKDLGEENFKALVL 24
                                                                                                                                                   ABM84995 standard; protein; 573 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2002; 2002US-0410259P.
12-SEP-2002; 2002US-0410260P.
                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2003; 2003WO-US028227
                                                                                                                                                                                                       (first entry)
Query Match 100.
Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene mapping.
                                                                                                                                                                                                                                                                                                                  WO2004023973-A2
                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                        RESULT 36
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Length 573;

100.0%; Score 123; DB 8;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to testing human cancer cells, comprising obtaining cancer cells from the patient and contacting the cell ex vivo with an antibody to the receptor for human albumin. The method is useful for testing human cancer cells in particular breast and prostate cancer cells. The present sequence is mature human serum albumin, HSA. The antiproliferative effect of HSA was assayed in an experiment included in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Testing human cancer cells, especially breast and prostate cancer cells, by contacting cancer cells obtained from biopsy of a patient ex vivo with antibody specific to human albumin receptor.
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                                                                                                                                                                                                                                                                                                                                                                         Human; serum albumin; HSA; cancer; cytostatic; breast cancer;
prostate cancer; anti-proliferative.
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                     Indels
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Misc-difference 241. .242
/note= "Encoded by GTCCACAGG"
                     0; Mismatches
                                                                                           25 DAHKSEVAHRFKDLGEENFKALVL 48
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0
                                                                                                                                                                                                              ABG72381 standard; protein; 584
                                                                                                                                                                                                                                                                                                                                        Mature human serum albumin #2.
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Similarity 100.0
24; Conservative
                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABX13582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
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                                                                                                                                                                                                                                                        ABG72381;
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Matches
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AAP93344
ID AAP93
XX
AC AAP93
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Mature protein of human serum albumin (see corresp. AAN90128). Used to make new N-terminal fragments which are used as plasma expanders, or as substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA encoding human normal serum albumin contained in plasmid - obtd. by culturing host transformed with expression vector comprising CDNA coding for albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA amino acid sequence of human serum albumin A (HSA-A) which is identical to that encoded by chromosomal DNA. Previous polypeptides produced from cDNA have one or more amino acids which differ from those
                                                                                                                                                                                                            New N-terminal fragments of human serum albumin - esp. useful as blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serum albumin A; pAT-pho-HSA-A; haemorrhagic shock;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 585;
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                                                                                                                        Senior PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 100.0%; Score 123; DB 1; Similarity 100.0%; Pred. No. 5.4e-11; 24; Conservative 0; Mismatches 0;
                                                                                                                        Geisow MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAHKSEVAHRFKDLGEENFKALVL 24
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                                                                                   (DELZ ) DELTA BIOTECHNOLOGY LTD
                88EP-00310000.
                                                    87GB-00025529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human normal serum albumin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89EP-00301731,
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                                                                                                                        Hinchliffe E,
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(first entry)
                                                                                                                                                            WPI; 1989-186464/26.
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Best Local Similarity
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                                                                                                                                                                                                                                    plasma expanders.
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                                                                                                                                                                              N-PSDB; AAN90128
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 585 AA;
                                                                                                                        Ballance DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-1989;
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                25-OCT-1988;
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                                                                                                                                                                                                                                                                                                                                                                              field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Artificial gene coding for authentic human serum albumin - constructed on the basis of codons most frequently used by chosen non-human host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human serum albumin; mature protein; new polypeptides; plasma expanders.
                                                     Sequence of mature human serum albumin (HSA) as encoded by artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                      Mature human serum albumin, artificial gene, oligonucleotide block, hypobolaemia, shock, hypoalbuminaemia.
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100.0%; Pred. No. 5.4e-11;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; pp. 11-16; 121pp; English.
                                                                                                                                                                                                                                                                                                                                        (SKAN-) SKANDIGEN AB.
(MAGY ) MTA SZEGEDI BIOLOG KOEZPONTI
(VEPE-) VEPEX CONTRACTOR LTD.
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 (revised)
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N-PSDB; AAN90997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 585 AA;
                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                      13-SEP-1988;
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 25-MAR-2003
23-JUN-1990
                                                                                                                                                                                                                                  22-MAR-1989
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25-MAR-2003
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Matches

RESULT 39 AAP90388

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BXRXXXXXXXXX

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of HSA-A produced from the chromosomal DNA, and may exhibit antigenicity when administered to humans. The HSA-A is used to treat haemorrhagic shock and hypoalbuminaemia. See also AAN90600. (Updated on 25-MAR-2003 to correct PI field.)
       8888888
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Sequence 585 AA;

0; Gaps Query Match 100.0%; Score 123; DB 1; Length 585; Best Local Similarity 100.0%; Pred. No. 5.4e-11; Matches 24; Conservative 0; Mismatches 0; Indels 0

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1 DAHKSEVAHRFKDLGEENFKALVL 24

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Search completed: August 19, 2005, 10:58:24 Job time : 165 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model protein ĕ

August 19, 2005, 10:45:00 ; Search time 56 Seconds (without alignments) 219.463 Million cell updates/sec Run on:

US-09-846-328B-1\_COPY\_2\_25 123 1 DAHKSEVAHRFKDLGEENFKALVL 24 Title: Perfect score:

Sequence:

1612378 seqs, 512079187 residues Searched:

Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		d			SUMMAKIES	
Result		Query				
No.	Score	Match	Length	DB	QI	Description
-	123	100.0	167	7	Q6UXK4	homo
7	123	100.0	396	~	Q81UK7	рошо
e	123	100.0	609	-	ALBU HUMAN	homo
4	117	95.1	609	~	Q68DNS	рошо
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9	111	90.2	417	7	Q86YG0	
7	110	89.4	9	н	ALBU MACMU	_
80	110	89.4	608	7	Q95VB7	
6	109	88.6	607	~	ALBU BOVIN	
10	106	86.2	608	٦	ALBU RAT	0 rattu
11	105	85.4	607	Н	ALBU_SHEEP	9 ovis a
12	100	81.3	607	-	ALBU_HORSE	P35747 equus cabal
13	98	79.7	205	~	Q8CG74	4 mus
14	98	79.7	608	Н	ALBU MOUSE	mus
15	98	79.7	608	~	Q8C7H3	mus mu
16	97	78.9	584	7	Q7YSG3	feli
	97	78.9	605	~1	ALBU PIG	ens
18	97	78.9	607	~	Q68NH7	BUB BC
	97	78.9	608	Н	ALBU FELCA	P49064 felis silve
20	97	78.9	608	7	6NDW9Q	Q6wdn9 cavia porce
21	97	78.9	609	Н	ALBU MERUN	
22	93	75.6	40	7	Q9TRAS	
23	93	75.6	608	н	ALBU RABIT	-
24	92	74.8	20	7	09 <u>0</u> 0 <u>x</u> 8	rattue
25	92	74.8	608	Н	ALBU CANFA	
56	89	72.4	30	~	Q7M3A0	•
27	87	70.7	20	~	Q9R4X7	_
28	87	70.7	25	7	Q9TRW8	_
59	84	68.3	583	~	Q6B3Z0	0
30	81	65.9	615	Н	ALBU CHICK	<del>.</del>
31	16	61.8	40	Н	ALB1_TRASC	P81188 trachemys s

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396 AA.

PRT;

PRELIMINARY;

QBIUK7 QBIUK7;

RESULT 2 OBIUK7 ID OB AC OB

Q9tr98 canis famil Q9prw0 struthlo ca Q8e111 streptococc Q8e728 streptococc P83729 naegleria f Q7m889 wolinella s P83517 neoceratodu Q8c77 mus musculu Q6c453 mus musculu Q7tt14 mus musculu Q6x177 rattus norv Q7nj13 gloeobacter Q83k42 shigella fl	
Q9TR98 Q9PRW0 Q8E1L1 Q8E1L2 Q8E728 Q7M8S9 ALBU NEOFS Q6ZQ53 Q7TT14 RBMC MQUSE Q6XLT7 Q6XLT7	
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## ALIGNMENTS

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curuwakii r.;

"The secreted protein discovery initiative (SPDI), a large-scale
if ffort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";

Genome Res. 13:2265-2270(2003).

RMBL; AY358313; AAQ89947.1; -.

RMSP; POST68; IAAO.

GO; GO:0005816; F:axrier activity; IEA.

RG); GO:0005816; F:carrier activity; IEA.

RG); GO:0005816; F:axrier activity; IEA.

RG); GO:0005816; F:axrier activity; IEA.

RG); GO:0005810; P:transport; IEA.

RG); 
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22897296; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE=22897296; PubMed=12975309; Baker K., Baldwin D., Brush J., Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chow B., Crimaldi C., Currell B., Deuel B., Dowd P., Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandler R., Watanabe C., Wieand D., Woodg K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang W., Zhang Z., Goddard A., Wood W.I., Godowski P.;
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ORFNames=UNG696;
Homo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altsuberg R.L., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A statchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,
B tapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Dosak S.A., McEvan F.J., McKernan K.J., Malek J.A., Guaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Makrayanski M.I., Skalska U., Samilus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC035969; AAH35969.1; -.
HSSP; P02768; 1NgU.
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P02768; 095574; Q13140; Q9P157; Q9P117; Q9UHS3; Q9UJZ0; 21-JUL-1986 (Rel. 01, Created)
01.APR-1990 (Rel. 14, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
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Created)
Last sequence update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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GO: 0005386; F:carrier activity; IEA.
GO: 0006810; P:transport; IEA.
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TISSUELNEE FROM N.A.

TISSUELINE=21398257; PubMed=12477932; DOI=10.1073/pnas.242603899;

TISSUELINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buerow K.H., Schamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buerow K.H., Schamefer C.P., Bhata N.K.,
A pitchul R.P., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,
A pitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., McKernan R.J., Marken B.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C. Manney D., Marra M.A.,
C. Grimwood S.J.M., Marra M.A.,
C. Marra M.A.,
C. Grimwood S.J.M., Marra M.A.,
C. Marra M.A.
Minghetti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W., Beattie W.G., Dugaiczyk A.;
Beattie W.G., Dugaiczyk A.;
Beattie W.G., Dugaiczyk A.;

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[2]
SRQUENCE FROM N.A., AND VARIANT LYS-420.

MEDLINE=82081882; Pubwed=6171778;
Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,
Najarian R.C., Seeburg P.H., Wion K.L.;

"The sequence of human serum albumin cDNA and its expression in E.
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MEDLINE=76187907; PubMed=1225573; DOI=10.1016/0014-5793(75)80242-0;
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Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.;
"Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver.",
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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ad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE-82105994; PubMed=6275391;
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Best Local Similarity 100.0%;
Matches 24; Conservative
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  RATER TRANSPORTED TO THE REPORT OF THE REPOR
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Urano Y., Watanabe K., Sakai M., Tamaoki T.;
"The human albumin gene. Characterization of the 5' and 3' flanking
regions and the polymorphic gene transcripts.";
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                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 222-229.
MEDLINE=76257808; PubMed=955075; DOI=10.1016/0014-5793(76)80496-6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Lysine residue 240 of human serum albumin is involved in high-affinity binding of bilirubin.";
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Pedint substitutions in albumin genetic variants from Asia.";
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Takahashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M.,
Satoh C., Neel J.V.;
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                                                                                                                                                                                                                                                                                                                                                                           Walker J.E.;
"Lysine residue 199 of human serum albumin is modified by
                                                                                                         Menaya J., Parrilla R., Ayuso M.S.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987)
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MEDLINE=78186630; PubMed=656055;
The chemistry and physiology of
Pergamon Press, New York (1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 25-44 AND 480-499
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                                                                 SEQUENCE OF 1-455 FROM N.A.
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                                                                                       TISSUE=Liver;
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"Two alloalbumins with identical electrophoretic mobility are produced
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"Structural characterization of a glycoprotein variant of human serum
albumin: albumin Casebrook (494 Asp-->Asn).";
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MEDLINE=92052189; PubMed=1946412;
Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E., Madison Y.-I., Amaki I., Putnam F.W.;
"Genetic variants of serum albumin in Americans and Japanese.";
Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
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"Albumin Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of human serum albumin whose precursor has an aberrant signal peptidase
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Skaryyota; Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primetes; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M., Minchiotti L., Putnam F.W.; A donor splice mutation and a single-base deletion produce two carboxyl-terminal variants of human serum albumin.";
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp779N1935.
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TISSUE=Liver;
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                                                                                                                                                                                                                                                                                    Rattus sp.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10118;
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Strausberg R.L., Fetingold E.N., Grouse L.H., Derged J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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                                                                                                     95.1%; Score 117; DB 2; Length 609; 95.8%; Pred. No. 1.3e-08; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  "Albumin in the cornea is oxidized by hydrogen peroxide.";
Cornea 11:567-572(1992).
HSSP; P02768; INSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                       Hypothetical protein.
SEQUENCE 609 Aa; 69402 MW; 3BA3AFF17BF99E94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  GO, GO:0005615; C:extracellular space; IEA.
GO; GO:0005386; F:carrier activity; IEA.
GO; GO:0006810; P:transport; IEA.
GO; GO:0006810; P:transport; IEA.
FICAPPO; IPR00204; Serum albumin.
Ffam; PF00273; Serum albumin; 1.
SEQUENCE 21 AA; 2429 MW; 26134A3D7CE29FAC CRC64;
                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.2%; Score 111; DB 2; L
100.0%; Pred. No. 2.9e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 AA.
                                                                                                                                                                                                                      21 AA
                                                                                                                                                1 DAHKSEVAHRFKDLGEENFKALVL 24
                                                                                                                                                           Created)
                                                                                                                                                                                                                                           Created)
InterPro; IPR000264; Serum albumin.
        Pfam; PF00273; Serum albumīn; 3.
PRINTS; PR00803; AFETOPROTEIN.
PRINTS; PR00802; SERUMALBUMIN.
PRODOM; PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
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Zhu L., Crouch R.K.;
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01-JUN-2003 (TrEMBLrel, 24,
01-JUN-2003 (TrEMBLrel, 24,
01-MAR-2004 (TrEMBLrel, 26,
                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26, 49 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.2%;
                                                                                                                Local Similarity 95.8 tes 23; Conservative
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Les 21; Conservative
                                                                                                                                                                                                                      PRELIMINARY;
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01-MAR-2004 (TrEMBLrel.
ALB protein.
Homo sapiens (Human).
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Sacraes M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Mozhan P.J., McKernan K.J., Malek J.A., Gunatane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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SEQUENCE FROM N.A.

MACHINE=93211971; PubMed=8460152;

MAEDLINE=93211971; PubMed=8460152;

MAEDLINE=93211971; PubMed=8460152;

MAEDLINE=93211971; PubMed=8460152;

MAEDLINE=93211971; PubMed=8460152;

MACHINE S.A., Sakamoto Y., Madison J.M., Davis E.M., Smith D.G.,

MACHINE S.A., Sakamoto Y., Madison J.M., Davis E.M., Smith D.G.,

MACHINE S.M., SAL, Sakamoto Y., Madison J.M., Smith D.G.,

MACHINE A. O.S., U.S.A. 90:2409-2413(1993).

MACHINE A. O.S., U.S.A. 90:2409-2413(1993).

MACHINE C. Natl. Acad. Sci. U.S.A. 90:2409-2413(1993).

MACHINE C. Natl. Machine A. M.S., Machine A. 
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041789; AAH41789.1; -
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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100.0%; Pred. No. 6.7e-08;
tive 0; Mismatches 0;
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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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GO; GO:0005615; C:extracellular space; IEA.

GO; GO:0005386; P:carrier activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR000264; Serum_albumin.
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SMART; SMOGLU3; ALBUMIN; 2.
PROSTIE; PS00212; ALBUMIN; 2.
SEQUENCE 417 AA; 47360 MW; 16E7.
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NCBI_TaxID=9544;
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Best Local Similarity
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF418550; AAL08579.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovinae; Bos
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                                                                                                                                                                                                                                                           Query Match
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Matches
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Albumin.
Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6183;
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Pred. No. 1.4e-07;
1; Mismatches 2; Indels
                                                                                                                                                                   EMBL; M90463; AAA36906.1; -.
PIR; A47391; A47391.
RISSP; P02768; IE7B.
IIICEPPC; IPR00103; Alphafetoprot.
IIICEPPC; IPR00103; Alphafetoprot.
IIICEPPC; Serum albumin.
PRINTS; PR008023; Serum albumin.
PRINTS; PR0080236; Serum albumin; 1.
PROSITE; PS00212; ALBUMIN; 3.
RROSITE; PS00212; ALBUMIN; 3.
COPPET; Lipid-binding; Metal-binding; Repeat; Signal.
NON TER.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity.
E45C871A670E740B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copper (By similarity). Bilirubin (Potential).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Osman A., Asahi H., Stadecker M.J., LoVerde P.T.;
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Serum albumin.
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       SIMILARITY: Contains 3 albumin domains.
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Albumin 2.
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Local Similarity 87.5%;
hes 21; Conservative
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SEQUENCE OF 1-32.
MEDLINE-80024278; PubMed=488109;
McGlllivray R.T.A., Chung D.W., Davie E.W.;
"Biosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of preproalbumin.";
Eur. J. Biochem. 98:477-485(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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MEDLINE=21195144; PubMed=11298124;
Hilger C., Grigioni F., De Beaufort C., Michel G., Freilinger J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deferminants of bovine serum albumin.", clin. Exp. Immunol. 123:387-394(2001).
                                                                                                                                                                                                                                                                                                                                                                                    Length 608;
HSSP; PO1768 1HKL.

GO; GO:000536; IHKL.

GO; GO:000536; F:carrier activity; IEA.

GO; GO:0006310; P:transport; IEA.

GO; GO:0006310; P:transport; IEA.

InterPro; IPR001703; Alphafetoprot.

InterPro; IPR00264; Serum albumin.

Pfam; PF00773; Serum albumin.

PRINTS; PR00803; AFETOPROTEIN.

PRINTS; PR00802; SERUMALBUMIN.

SMART; SM01013; ALBUMIN. 3.

PROSITE; PS00212; ALBUMIN. 2.

SEQUENCE 608 AA; 68225 MW; ESEABB20BIC66E54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barry T., Power S., Gannon F.; "The bovine serum albumin mRNA."; Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANT THR-214.
Wu H.T., Huang M.C.;
"The complete cDNA sequence of bovine serum albumin.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALBU BOVIN STANDARD; PRT; 607 AA. P02769; 002787; 21-JUL-1986 (Rel. 01, Created) 25-007-2004 (Rel. 33, Last sequence update) 25-007-2004 (Rel. 45, Last annotation update) Serum albumin precursor (Allergen Bos d 6) (BSA)
                                                                                                                                                                                                                                                                                                                                                                                       Score 110; DB 2;
Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT THR-214 TISSUE=Liver;
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MEDLINE=77134075; PubMed=843354;
                                                                                                                                                                                                                                                                                                                                                                                             89.4%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 83.3
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                        SMART; SM00103; ALBUMIN; 3.
SMOSITE; PS00212, ALBUMIN; 3.
Allergen; Copper; Direct procein sequencing; Lipid-binding; Metal-binding; Polymorphism; Repeat; Signal.
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Missing (in Ref. 10).
C -> K (in Ref. 8).
KP -> PC (in Ref. 8).
N -> D (in Ref. 8).
ST -> TS (in Ref. 8).
K -> R (in Ref. 8).
ST -> ES (in Ref. 9).
SE -> ES (in Ref. 8).
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Albumin 1.
Albumin 2.
Albumin 3.
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or send an email to license@isb-sib.ch)
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                                                                                                                                          InterPro; IPR001703; Alphafetoprot.
                                                                                                                                                                                   Pfam; PF00273; Serum albumīn; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
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                               EMBL; M73993; AAA51411.1; -.
EMBL; X58989; CAA41735.1; -.
EMBL; Y17769; CAA76847.1; -.
EMBL; AF542068; AAN17824.1; -.
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607 AA;
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Matches 20; Conserv
                                                                                                                              P02768; 1HK1
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Brown J.R.;

Structure of serum albumin: disulfide bridges.";

Fed. Proc. 33:1389-1389(1974).

In Table Specify for water, Ca(2+), Na(+), K(+), fatty acids, hordnense, blirtubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

SUBCELLULAR LOCATION: Secreted.

FALISRGEN: Causes an allergic reaction in human.

SIMILARITY: Belongs to the ALB/AFP/VDB family.

SIMILARITY: Contains 3 albumin domains.
                                                                                                                          Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.; Rapid confirmation and revision of the primary structure of bovine serum albumin by ESIMS and Frit-FAB LC/MS."; Biochem. Biophys. Res. Commun. 173:639-646(1990).
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MEDIATRE=88267456; PubMed=3389500;
MEDIATRE=88267456; PubMed=3389500;
HBich J.C., Lin F.P., Tam M.F.;
"Electroblotting onto glass-fiber filter from an analytical isochectrofocusing onto glass-fiber filter from an analytical forelectroblotting onto grass-fiber filter from an analytical isochectrofocusing gel: a preparative method for isolating proteins for N-terminal microsequencing.";
Anal. Biochem. 170:1-8(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 163-172.

PubMed=2474609;

Carraway R.E., Cochrane D.E., Boucher W., Mitra S.P.;

"Structures of histamine-releasing peptides formed by the action of acid proteases on mammalian albumin(s).";

J. Immunol. 143:1680-1684(1989).
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PubMed=2279503;
Strawich E., Glimcher M.J.;
"Tooth 'enamelin' identified mainly as serum proteins. Major 'enamelin' is albumin.";
Patterson J.E., Geller D.M.; "Bovine microsomal aequence of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 402-433.
MEDLINE=82023364; PubMed=7283978;
Reed R.G., Putnam F.W., Peters T. Jr.;
"Sequence of residues 400-403 of bovine serum albumin.";
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                                                      Biochem. Biophys. Res. Commun. 74:1220-1226(1977)
                                                                                           AND REVISIONS TO 118-119 AND 180,
                                                                                                                                                                                                                                                                                                                                                         to the PIR data bank
                                                                                                                                                                                                                                                             "Structure of bovine serum albumin."; Fed. Proc. 34:591-591(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vilbois F.;
Submitted (AUG-1998) to Swiss-Prot.
                                                                                                             MEDLINE=91083649; PubMed=2260975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 191:47-56(1990)
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                                                                                                                                                                                                                                                                                                                                           Brown J.R.;
Submitted (APR-1975)
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A Aoyaqi Y., Ikenaka T., Ichida F.;
Aoyaqi Y., Ikenaka T., Ichida F.;
Cancer Res. 38:3483-3486(1978).
Cancer Res. 38:3483-3486
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                                                                                                                                     MEDIJUE=77249667; PubMed=83447; Strauss A.W., Rodkey J.A., Alberts A.W.; Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.; "Rat liver pre-proalbumin: complete amino acid sequence of the pre-priese. Analysis of the direct translation product of albumin messenger RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-76260153; PubMed=956149;
Isemura S., Ikenaka T.;
"Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino acid sequences of four fragments.";
J. Biochem. 79:1183-1196(1976).
                               MEDLINE-81223722; PubMed=7017712;
Sargent T.D., Yang M., Bonner J.;
"Nucleotide sequence of cloned rat serum albumin messenger RNA.";
Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carraway R.E., Mitra S.P., Cochrane D.E., "Structure of a biologically active neurotensin-related peptide obtained from pepsin-treated albumin(8)."; J. Biol. Chem. 262:5968-5973(1987).
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Interpro; IPR001703; Alphafetoprot.
Interpro; IPR001204; Serum albumin.
Pfam; PF00273; Serum albumīn; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum albumin.
SMART; SM00103; ALBUMIN.
                                                                                                                                                                                                                                               Biol. Chem. 252:6846-6855(1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Plasma;
MEDLINE=87194805; PubMed=2437111;
                                                                                                                                 SEQUENCE OF 1-38, AND PROCESSING.
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Rat-heart-2DPAGE; P02770; -.
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                                                                                                                                                                                                                                                                                                                                                                                  Biochem. 83:35-48(1978)
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   [1]
SEQUENCE PROM N.A.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis
NCBI_TaxID=9940;
Copper; Direct protein sequencing; Lipid-binding; Metal-binding;
Repeat; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 106; DB 1; Length 608;
Pred. No. 5.8e-07;
4; Mismatches 1; Indels
                                                              Serum albumin.
Neurotensin-related peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                  5BB497A282411AB7 CRC64;
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01-APR-1990 (Rel. 14, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Y -> L (in Ref.
                                                                                                                                                  By similarity.
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Albumin 3.
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MEDLINE=90098888; PubMed=2602160;
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Best Local Similarity
Matches 19; Conserv
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25 DTHKSEIAHRFNDLGEKHFKGLVL 48
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75.0%;
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Mus musculus (Mouse).
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es 18; Conserv
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Q8CG74;
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  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93345495; PubMed=8344282;
Ho J.X., #Glowachuk E.W., Norton B.J., Twigg P.D., Carter D.C.;
"X-ray and primary structure of horse serum albumin (Equus caballus)
at 0.27-nm resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 215:205-212(1993).
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                85.4%; Score 105; DB 1; Length 607; 79.2%; Pred. No. 7.7e-07;
                                                                                                                                                                                                                                                                                                                                                               84979A87F8B86596 CRC64;
                                                                                                                                     Copper; Lipid-binding; Metal-binding; Repeat; Signal. SIGML 1 18 By similarity. 24 By cimilarity. CHAIN 25 607 Serum albumin.
                                                                                                                                                                                                   similarity).
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01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serum albumin precursor (Allergen Equ c 3).
                                                                                                                                                                                                                   similarity.
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Similarity.
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similarity.
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2; Mismatches
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By similarity
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                                                             HSSP, P02768; 1HK1.
InterPro; IPR001703; Alphafetoprot.
InterPro; IPR001204; Serum albumin.
Pfam; PP00273; Serum albumin; 3.
PRINTS; PR00802; SERÜMALBUMIN;
ProDom; PD002486; Serum albumin; 1.
SWART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
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                                             EMBL; X17055; CAA34903.1; -.
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nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                   Equus caballus (Horse)
                                                       S06936; ABSHS.
                                                                                                                                                                                                                                                                                                                                                               607 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9796;
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DR EMBL; X74045; CAA52194.1; -..

DR PIR, S34053; ABHOS.

DR PIRSP; BO2768; HIKI.

DR PROPOSTS; Serum albumin, 3.

DR PRINTS; PRO00264; Serum albumin, 3.

DR PRODOM; PRODOM; Serum albumin, 1.

DR RANT; SM00103; ALBUMIN; 3.

DR Allergen; Copper; Lipid-binding; Metal-binding; Repeat; Signal.

FT SIGNAL

DOMAIN 25 607 Serum albumin.

FT CHAIN 25 607 Serum albumin.

DOMAIN 25 404 Albumin.

211 396 Albumin 2.

COpper (By similarity).
binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, blirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

SUBCELLULAR LOCATION: Secreted.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                   -i- TISSUE SPECIFICITY: Plasma.
-i- ALLERGEN: Causes an allegic reaction in human. Binds IgE
-i- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-i- SIMILARITY: Contains 3 albumin domains.
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Pred. No. 4.2e-06;
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Last annotation update)
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Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                        SEQUENCE FROM N.A.
STRAINS 1976 SECULER;
STRAINS 1976 SECULER;
STRAINS TO SECULE T., Gabant P., Szpirer J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJZ77794; CAC81903.1; -.
HSSP; POZ768; 1HK.
GO, GO:0005615; C:extracellular space; IEA.
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MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C., Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 2.7e-06;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AA; 23624 MW; 0A982E85C7474BF9 CRC64;
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01-APR-1988 (Rel. 07, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                GO; GO: 00055(15) C: extracellular space; IEA.
GO; GO: 0005386; F: carrier activity; IEA.
GO; GO: 0005386; F: carrier activity; IEA.
GO; GO: 0005386; F: carrier abumin.
Pfam; PF00273; Serum albumin.
PRINTS; PR00802; SERUMALBUMIN.
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Mus musculus (Mouse).
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70.88;
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Best Local Similarity
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          NCBI_TaxID=10090;
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SEQUENCE
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STATE = VENDER = LANGEY, and LYSE;

WEDLINE = 2238827; PubMed=1247922; DOI=10.1073/pnas.242603899;

A Klauener R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Bookins R.P., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

A Altschenko L., Marueina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wokernan K.J., Malek J.A., Gunaratne P.H.,

Roask S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Rodriques S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield N., Schein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb.ch).
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Mouse liver protein database: a catalog of proteins detected by two-dimensional gel electrophoresis.";
Electrophoresis 13:970-991(1992).
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water. (ca(2+), Na(+), K(+), fatty acids, bromones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SINELLUIAR LOCATION: Secreted.
-!- SINELLUIAR LOCATION: Secreted.
-!- SINELLUIAR LOCATION: A cateform.
-!- SINELLUIAR LOCATION: A cateform.
-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 99-516 FROM N.A.
MEDILNE=88316123; PUMPdc=2452956;
Minghetti P.P., Law S.W., Dugaiczyk A.;
"The rate of molecular evolution of alpha-fetoprotein approaches that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=902659606; PubMed=1971802; DOI=10.1016/0378-1119(90)90030-U; Boccaccio C., Deschatrette J., Meunier-Rotival M.; Empty and occupied insertion site of the truncated LINE-1 repeat Jocated in the mouses serum albumin-encoding gene."; Gene 88:181-186(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney, and Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of pseudogenes.";
Mol. Biol. Evol. 2:347-358(1985)
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EMBL; BC049971; AAH49971.1;
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1 DAHKSEVAHRFKDLGEENFKALVL 24
Meth. Enzymol. 303:19-44(1999).
                                                                                                             SEQUENCE FROM N.A.
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STRAIN=CS7BL/60; TISSUE=Liver;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                 Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched
library, clone:C730030P03 product:albumin 1, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                ProDom; PD002486; Serum_albumin; 1.
PROSTIR; PS00212; ALBUMIN; 3.
Copper; Direct protein sequencing; Lipid-binding; Metal-binding;
Repeat; Signal.
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Albumin 2.
Albumin 3.
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                               MGD; MGI:87991; Albl.
InterPro; IPR001703; Alphafetoprot.
InterPro; IPR001264; Serum albumin.
Pfam; PF00773; Serum albumin; 3.
PRINTS; PR00802; SERUMALBUMIN.
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EMBL; M16111; AAA37190.1; -. EMBL; X13060; CAA31458.1; -. PIR; A05139; A05139.
                   HSSP; PO2768; 1HK1.
SWISS-2DPAGE; P07724; MOUSE.
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 70.8<sup>1</sup>
....hes 17; Conservative
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SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

A bukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

A Hori F., Indtani X., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Gano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRANT-CSTBL/GJ TISSUE-Liver;
STRANT-CSTBL/GJ TISSUE-Liver;
The FANTOW COMSOCTIUM.
THE RIKEN GENOME Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUB=Liver; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Medeline=20499374; PubMed=11042159; DOI=101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Shibata K., Itoh M., Forno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shibata K., Itoh M., prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Liver;
STRAIN=C57BL/6J; TISSUE=Liver;
STRAIN=C57BL/6J; TISSUE=Liver;
STRAIN=C9013; Pubmed=11076861; DOI=10.1101/gr.152600;
MEDLINE=2039013; Pubmed=11076861; DOI=10.1101/gr.152600;
A Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., A Konno H., Akiyama J., Nibahi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nacamura S., Hazama M., Nishine T., Harada A., Yamamonco R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Matshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Ackazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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                                                                                                                                                                       'Functional annotation of a full-length mouse cDNA collection.";
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SEQUENCE FROM N.A.
STRAIN=CSTBL/6J; TISSUE=Liver;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANYOM CONSORTIUM;
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Pred. No. 8.4e-06;
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InterPro; IPR000264; Serum albumin.
Edm, PR000273; Serum albumin; 3.
PRINTS; PR00803; AFETOPROTEIN.
PRINTS; PR00802; SERUMALBUMIN.
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ProDom; PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
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SEQUENCE 608 AA; 68722 MW;
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"Nuclectide sequence of porcine liver albumin.";
"Nuclectide sequence of porcine liver albumin.";
"Nuclectide Res. 16:9045-9045(1988).
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good
binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
hordones, bilirubin and drugs. Its main function is the regulation
of the colloidal osmotic pressure of blood.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- TSUBS PRECIFICITY: Plasma.
-!- SIMILARITY: Belongs to the ALB/APP/VDB family.
-!- SIMILARITY: Contains 3 albumin domains.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Felidae, Felis.
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
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Reininger R., Swoboda I., Bohle B., Hauswirth A.W., Valent P.,
Rumpold H., Valenta R., Spitzauer S.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ48/PG77; CAD32275.1; -.
HSSP; P02768; 1E7B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.9%; Score 97; DB 2; Length 584; Best Local Similarity 70.8%; Pred. No. 1.1e-05; Matches 17; Conservative 5; Mismatches 2; Indels
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                                                                                                                                                                                                                                    Created)
Last sequence update)
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                                                                                                                                                                                 584 AA.
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                                                                                                                                                                           PRELIMINARY;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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3E556B0DDIA1F4FF CRC64;
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18.9%; Score 97; DB 1; Length 60:
Best Local Similarity 75.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                             PERMIT PRODUCES, Serum albumin.
PERMIT PRO0273; Serum albumin.
PRINTS; PRO0802; SERUMALBUMIN.
PRODUCT PRO0013; ALBUMIN.
PROSITE; PSO0213; ALBUMIN; 3.
PROSITE; PSO0212; ALBUMIN; 3.
COPPET, Lipid-binding; Metal-binding; Repeat; Signal.
NON TER
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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By similarity.
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By similarity.
Serum albumin.
Albumin 1.
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Sun S., Deng J., Zhou Y., Lu J., Wu X.;
"Porcine serum albumin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Albumin 2.
Albumin 3.
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562
605 AA;
                                                                                                                                                                                                                                 PIR; S01382; ABPGS.
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Gaps

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GGWDN9;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Preproalbumin precursor.
Preproalbumin precursor.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Caviidae; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                  78.9%; Score 97; DB 1; Length 608; 70.8%; Pred. No. 1.2e-05; ive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mihaylova-Todorova S., Choe S.M., Westfall D.P.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX294645; AAQ20088.1; -.
HSSP; P02768; 1AO6.
                                                                                                                                                                                                                                                                                                                                    07E629CAC5F60E5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005615; C:extracellular space; IEA.
GO; GO:0005615; C:extracellular space; IEA.
GO; GO:000510; P:ramisport; IEA.
InterPro; IPR001703; Alphafetoprot.
InterPro; IPR000264; Serum albumin.
PRINTS; PR00803; AFETOPROTEIN.
PRINTS; PR00802; SERUMALBUMIN.
PRODOT: SMEUMALBUMIN.
PRODOT: SMEUMALBUMIN.
PRODOT: SMEUMALBUMIN.
PRODOT: SMEUMALBUMIN.
PROSTIE; PS00212; ALBUMIN; 3.
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25 EAHQSEIAHRFNDLGEEHFRGLVL 48
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nes 17; Conservative
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608 AA;
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TISSUE=Liver;
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                      SULFID
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Q6WDN9
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R PIR; JC4660; S5763.
R HSSP; PO2768; IE7B.
R INTERPORTOROUS, ESTUM albumin.
DR PRO0273; Serum albumin; 3.
DR PRINTS; PR0002486; Serum albumin; 1.
DR PRODOM; PD002486; Serum albumin; 1.
DR PROSITE; PS00212; ALBUNIN; 3.
DR PROSITE; PS00212; ALBUNIN; 3.
DR PROSITE; PS00212; ALBUNIN; 3.
FR Allergen; Copper; Lipid-binding; Repeat; Signal.
FT SIGNAL

1 18 By similarity.
19 24 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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                                                                                                                                                                                                 Length 607;
                                                                                                                                                                                             'Match 78.9%; Score 97; DB 2; Length 607 Local Similarity 75.0%; Pred. No. 1.2e-05; Lonservative 3; Mismatches 3; Indels
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY665543; AAT98610.1; -.
InterPro; IPR00264; Serum albumin.
Pfam; PF00273; Serum albumin.
ProDom; PR0023; Serum albumin; 3.
PRODOM; PR002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
SRQUENCE 607 AA; 69691 MW; 7B8DA13543CA99D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- ALLERGEN: Causes an allergic reaction in human.
-i- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-i- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
02-UJ-2004 (Rel. 44, Last annotation update)
Serum albumin precursor (Allergen Fel d 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serum albumin.
Albumin 1.
Albumin 2.
Albumin 3.
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P49064;
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ALBU FELCA
DT 01-FEB-

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                                                          Query Match 78.9%; Score 97; DB 2; Length 608; Best Local Similarity 75.0%; Pred. No. 1.2e-05; Matches 18; Conservative 3; Mismatches 3; Indels
508 albumin.
68889 MW; BBD510A78D0261BA CRC64;
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REVISIONS TO 322-323 AND 506-507. Sheffield W.P.;
                                                                                                                                                                                                      Antagonist protein (Fragment).
Oryctolagus cuniculus (Rabbit).
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70.8%;
                    78.9%;
                    Query Match
Best Local Similarity 78.3
Matches 18; Conservative
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SEQUENCE
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SEQUENCE FROM N.A.

STRAIN-MGS IDR; TISSUB=Liver;

MEDLINE-pala16663; PubMed=4955485;

MY Yoshida K., Seto-Ohshima A., Sinohara H.;

"Sequencing of cDNA encoding serum albumin and its extrahepatic synthesis in the Mongolian gerbll, Meriones unguiculatus.";

"Sequencing of cDNA encoding serum albumin, the main protein of plasma, has a good the DNA Res. 4:351-354(1997).

"I DNA Res. 4:351-354(1997).

"I DNA Res. 4:351-1354(1997).

"I DNA Res. 4:351-1354(1997).

"I FUNCTION: Serum albumin, the main protein of plasma, has a good hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

"I SUBCELULAR LOCATION: Secreted.

"I SUBCELULAR LOCATION: Secreted.

"I ISSUE SPECIFICITY: Plasma.

"I ISSUE SPECIFICITY: Belongs to the ALB/AFP/VDB family.

"I SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way much profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                       Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AB006197; BAA21765.1; -.
PIR, JC5838; JC5838.
HSSP; P02768; 1B7B.
InterPro; 1PR001703; Alphafetoprot.
InterPro; 1PR000264; Serum albumin.
Pfam, PF00273; Serum albumin. 3.
PRINTS; PR00802; SERUMALBUMIN.
I PRODOM; P002486; Serum albumin; 1.
SWART; SW00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
COPPER; Lipid-binding; Metal-binding; Repeat; Signal.
                                 (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 44, Last annotation update)
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By similarity.
Serum albumin.
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Albumin 3.
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             PRT;
             STANDARD;
                                                                     Serum albumin precursor.
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                                 15-JUL-1998
                                                        05-JUL-2004
             ALBU MERUN
035090;
                                                                                Name=ALB;
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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"Purification, amino-terminal sequence and functional properties of the yotosolic protein from heart muscle capable of modulating calcium transport across the sarcoplasmic reticulum in vitro.";
Mol. Cell. Biochem. 132:7-14(1994).
Hissp: P02768; INSU.
GO; GO:0005615; C:extracellular space; IEA.
GO; GO:0005810; P:transport; IEA.
GO; GO:0005810; P:transport; IEA.
Histp: P00273; Serum albumin.
Pfam; PF00273; Serum albumin.
Pfam; PF00273; Serum albumin; Histp: BATE0B69C6CE858C CRC64;
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Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
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MEDLINE=97275135; PubMed=9129029;
Syed S., Schupler P.D., Kulczycky M., Sheffield W.P.;
Syed stricthrombin activity and delayed clearance from the "Potent antithrombin activity and delayed clearance from the circulation characterize recombinant hirudin genetically fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 2.6e-06;
4; Mismatches 3; Indels
609 AA; 68940 MW; 9CASF97F67EF1A48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                         Score 97; DB 1; Len
Pred. No. 1.2e-05;
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29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608 AA.
                                                                                                                                                                                                                                                                                                                                                                  40 AA
                                                                                                             3; Mismatches
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                                                                                                                                                                                                27 AHKSEIAHRYKDLGEKYFKGLVL 49
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                                                                                                                                                                    2 AHKSEVAHRFKDLGEENFKALVL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
MEDLINE=94359514; PubMed=8078511;
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Gaps

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1; Indels

Score 92; DB 2; I Pred. No. 1.8e-06;

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MEDINE-96087830; PubMed-8587647;
Onozuka M., Imai S., Isobe T., Yen C.T., Watanabe K.;
Onozuka M.; Imai S., Isobe T., Yen C.T., Watanabe K.;
Purfication and characterization of a novel 70-kDa brain protein associated with seizure activities.";
Neurochem. Res. 20:901-905(1995).
HSSP: P02768; 1N5U.
SEQUENCE 20 AA; 2381 MW; 534A23C0F9F70F7D CRC64;
                                                                                                 74.8%; Scor.
80.0%; Pred. No. 1...
                                                                                                                                           1 DAHKSEVAHRFKDLGEENFK 20
                                                                                           Query Match
Best Local Similarity 80.00
Local 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dog heart proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 25-38.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
   NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergen.";
                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn M.
                                                                                                                                                                                               ALBU CANFA
                                                                                                                                                                                        RESULT 25
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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OGOX8...
OGOX8...
OGOX8...
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 11, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 21, Last amotation update)
O1-UNN-2002 (TrEMBLrel. 21, Last amotation update)
TO kDa seizure activity-linked albumin-like glycoprotein (Fragment).
Rattus sp. ..
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                               EMBL, 1018344; AABS8347.2; -..

RESP, PO2768; 1E7B.

InterPro; IPR000264; Serum albumin.

PERM, PR00273; Serum albumin; 3.

PRINTS, PR0080020; SERUMALBUMIN; 1.

PRODOM; P0002486; Serum albumin; 1.

R SMART; SM00103; ALBUMIN; 3.

R CORPET, Lipid-binding; Metal-binding; Repeat; Signal.

T GRNAL 1 18 By similarity.

T PROPEP 19 24 By similarity.

T PROPEP 25 608 Serum albumin.

T DOMAIN 25 608 Albumin 1.

T DOMAIN 212 397 Albumin 2.

T DOMAIN 25 Albumin 3.
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similarity.
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582
608 AA;
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ses 17; Conserv
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TISSUE-Liver;
MEDIINE-20148667; PubMed-10669848; DOI=10.1016/S0091-6749(00)90077-0;
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"Isolation, amino acid sequence and copper(II)-binding properties of
peptide (1-24) of dog serum albumin.";
J. Biol. Chem. 249:5872-5877(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn M.J., Corbett J.M., Wheeler C.H.; "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Allergy Clin. Immunol. 93:614-627(1994).
-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         raminiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Salivary gland;
MEDLINE=94201492; PubMed=7512102;
Spitzauer S., Schweiger C., Sperr W.R., Pandjaitan B., Valent P.,
Muehl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;
"Molecular characterization of dog albumin as a cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pandjaitan B., Swoboda I., Brandejsky-Pichler F., Rumpold H., Valenta R., Spitzauer S.; "Escherichia coli expression and purification of recombinant dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                         ALBU CANFA STANDARD; PRT; 608 AA. P49822; 077705; Q9TSZ4; 01-0CT-1996 (Rel. 34, Created) CCT-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Serum albumin precursor (Allergen Can f 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           albumin, a cross-reactive animal allergen."; J. Allergy Clin. Immunol. 105:279-285(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 25-48.
MEDLINE=75011422; Pubmed=4414013;
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1 EAHKSEIAHRFKDLGEQXFK 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Beagle; TISSUE=Liver;
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Tachyglossus autoatus (Australian echidna).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Monotremata, Tachyglossidae, Tachyglossus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
66 kDa SEROREACTIVE protein/serum albumin homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE 94343500; PubMed=8064836; Deshpande R.G.; Marakar R.G.; Deshpande R.G., Khan M.B., Bhat D.A., Navalkar R.G.; Purification and partial characterisation of a novel 66-kDa seroreactive protein of Mycobacterium tuberculosis H37Rv."; J. Med. Microbiol. 41:173-178(1994). SEQUENCE 20 AA; 2393 MW; 534A232072870F7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 89; DB 2; Length 30;
Pred. No. 7.5e-06;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 AA; 3482 MW; 01AEA775ECCB474C CRC64;
                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                        SEQUENCE.
Teahan C.G., McKenzie H.A., Griffiths M.;
"Some monotreme milk "whey" and blood proteins.";
Comp. Biochem. Physiol. 99:99-118(1991).
PIR, Belsil; Belsil.
HSSP; P02768; 1BKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.7%; Score 87; DB 2; I
80.0%; Pred. No. 9.7e-06;
tive 1; Mismatches 3;
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                  30 AA.
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GO; GO:0005615; C:extracellular space; IEA.
GO; GO:0005386; F:carrier activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000264; Serum_albumin.
Pfou?73; Serum_albumin.
                                                                                                                               (Fragment
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                                                             Created)
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                                                                                 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Serum albumin, milk-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Query Match
Best Local Similarity 66.77,
Best Local Similarity 66.77,
Best Local Similarity
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                  PRELIMINARY;
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                    Q7M3A0 PRELIMINARY
Q7M3A0;
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                            NCBI_TaxID=9261;
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SEQUENCE
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Q9TRW8
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27M3A0
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  main function is the regulation
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By similarity.

By similarity.
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REMBL; X177346; AAB30434.1; -...
REMBL; S72946; AAB30434.1; -...
RESP; PO2768; 1E78.
RESP; PO02768; 1E78.
RESP; PO0273; Serum albumin.
Prem, PPO0273; Serum albumin.
REINTS; PRO0602; SRRÜMALBUMIN.
REINTS; PRO0103; ALBUMIN.
REINTS; PRO0103; ALBUMIN.
REINTS; PRO0112; ALBUMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.8%; Score 92; DB 1; Length 608; 66.7%; Pred. No. 6.5e-05; ive 6; Mismatches 2; Indels
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-> VV (in Ref. 5).
-> E (in Ref. 1).
3CF1C8FF7DD8FC06 CRC64;
                                                               TISSUE SPECIFICITY: Plasma.
ALLERGEN: Causes an allergic reaction in human.
SIMILARITY: Belongs to the ALB/APP/VDB family.
SIMILARITY: Contains 3 albumin domains.
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(in Ref. 2).
hormones, bilirubin and drugs. Its main fur of the colloidal osmotic pressure of blood SUBCELLULAR LOCATION: Secreted.
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Albumin 2.
Albumin 3.
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Metal-binding; Repeat; Signal.
ا Potential.
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Matches 16; Conservative
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608 AA;
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DOMAIN
DOMAIN
DOMAIN
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Gaps

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Last sequence update)
Last annotation update)
25 AA
                    Created)
                   (TrEMBLrel. 13, 0
(TrEMBLrel. 13, 1
(TrEMBLrel. 26, 1
                    01-MAY-2000
01-MAY-2000
01-MAR-2004
             Q9TRW8
   22555
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Gaps

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Length 20; 3; Indels

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TISSUE=Liver;
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                       ALBU_CHICK
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                                                                                                                                                              MEDLINE-91330574; PubMed=1868684; Grane P.E.; Grigor M.R., Bennett B.L., Carne A., Cowan P.E.; Whey proteins of the common brushtail possum (Trichosurus vulpecula): isolation, characterization and changes in concentration in milk during lactation of transferrin, alpha-lactalbumin and serum albumin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Lazar J., Rasmussen B., Greenwood D.R., Bang I.-S., Prestwich G.D.,
"Elephant Albumin: A Multi-purpose Pheromone Shuttle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Proboscidea, Elephantidae, Elephas.
NCBI_TaxID=9783;
                       Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
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Pred. No. 0.00094;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.7%; Score 87; DB 2; Length 25; 75.0%; Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chem. Biol. 0:0-0(2004).

EMBL; AY684122; AAT90502.1; -
GO; GO:0005612; C:extracellular space; IEA.
GO; GO:0005386; F:carrier activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000054; Serum albumin.
PROMOT3; Serum albumin.
PROMOT3; PREWMALBUMIN.
ProDom; PD002486; Serum albumin; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 AA.
                                                                                                                                                                                                                                                                                                                                                                   Comp. Biochem. Physiol. 98B:451-459(1991).
HSSP; P02768; 109X.
GO; GO:0005615; C:extracellular space; IEA.
GO; GO:0005816; F:carrier activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000264; Serum_albumin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 HKSEVAHRFKDLGEENFKALVL 24
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68.2%;
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Best Local Similarity 68.2%,
Best Local 15, Conservative
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Serum albumin (Fragment)
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                                                                                                        NCBI TaxID=9337;
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Quirce S., Maranon F., Umpierrez A., de las Heras M.,
Quirce S., Maranon F., Umpierrez A., de las Heras M.,

Rernandez-Caldas E., Sastre J.;
Rernandez-Caldas E., Sastre J.;
Thicken serum albumin (Gal d 5*) is a partially heat-labile inhalant
and food allergen implicated in the bird-egg syndrome.";
Allergy 56:754-762(2001).
C. - FUNCTION: Serum albumin, the main protein of plasma, has a good
binding capacity for water, Ca(2+), Na(+), fatty acids,
binding capacity for water, Ca(2+), Na(+), fatty acids,
c. - FUNCTION: Serum albumin, the main protein of plasma, has a good
binding capacity for water, Ca(2+), Na(+), fatty acids,
c. - I- FUNCTION: Secreted.
C. - SUBCELLULAR LOCATION: Secreted.
C. - ALLERGEN: Causes an allergic reaction in human. Binds IgE.
C. - ALLERGEN: Causes an allergic reaction in human. Binds IgE.
C. - ALLERGEN: Causes an allergic reaction in human. Binds IgE.
C. - SIMILARITY: Belongs to the ALB/APP/VDB family.
C. - SIMILARITY: Belongs to the ALB/APP/VDB family.
C. - SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83161037; PubMed=6187737; Hache R.J.C., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G.; Hache R.J.C., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G.; "The 5' noncoding and flanking regions of the avian very low density apolipoprotein II and serum albumin genes. Homologies with the egg
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen A.M., Geller D.M.; "Chicken microsomal albumin: amino terminal sequence of chicken
                                                                                                                                                                                                                                                                                                                                  Cassady A.I., Salklld C.K., Baverstock P., Wallace J.C., Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
                                       01-NOV-1990 (Rel. 16, Created)
01-AUC-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serum albumin precursor (Alpha-livetin) (Allergen Gal d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 78:1060-1066(1977).
615 AA
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InterPro; IPR000264; Serum albumin.
Pfam; PF00273; Serum albumin; 3.
PRINTS; PR00802; SERUMALBUMIN;
ProDom; PD002486; Serum albumin; 1.
PROSITE; SM00103; ALBUMIN; 3.
PROSITE; PS002121; ALBUMIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                white protein genes.";
J. Biol. Chem. 258:4556-4564(1983).
[3]
SEQUENCE OF 19-30.
MEDLINE=78019943; PubMed=911327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLERGENIC PROPERTIES.
MEDLINE=21381307; PubMed=11488669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X60688; CAA43098.1; -. EMBL; V00381; CAA23680.1; -.
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STANDARD;
                                                                                                                                                     Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Gaps

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Metal-binding.

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MEDITNE=94341467; PubMed=8063009; DOI=10.1016/0020-711X(94)90114-7; Kuhn C.R., Naude R.J., Travis J., Oelofsen W.; Travis J., Oelofsen W.; Travis J., Oelofsen M.; Travis J., Oelofsen J., J.; Serun of the ostrich (Struthio camelus)."; SEQUENCE JO AA; 3557 MW; 7775AA786EB30AC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Čhordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
Miller M.J., Parmelee D.C., Benjamin T., Sechi S., Dooley K.L.,
Kadlubar F.F.;
                                                                                                                      Score 76; DB 1; Lengtn wv, Pred. No. 0.00085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.7%; Score 71; DB 2; Length 17; 70.6%; Pred. No. 0.0019; cive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WAR-1995) to the EMBL/GenBank/DDBJ databases.
17 AA; 2024 MW; 1D39F70F7D23B269 CRC64;
      18SP; POZ768; 1E7H.
INTERPRO; IPR000264; Serum albumin.
Pfam, PP00273; Serum albumin; 1.
PROSITE; PS00212; ALBUMIN; PARTAL.
COPPET; Direct protein sequencing; Lipid-binding; M.
COPPET; Birect 4 COPPET (By similarity)
                                                                                                     40 AA; 4682 MW; SFAC9E49E2789BB0 CRC64;
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-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
                                                                                                                                                                                                                                                                                                                        sequence update)
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Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                  17 AA.
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                                                                                                                                                             1; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Latt sequen
01-MAR-2002 (TrEMBLrel. 20, Last annota
Alpha 1-proteinase inhibitor (Fragment)
struthio camelus (Ostrich)
                                                                                                                                                                                                                                                                                                             Created)
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EAYKSEIAHRYNDLGEE 17
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59.18;
                                                                                                                                   61.8%;
63.6%;
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01-MAY-2000 (TrEMBLrel. 13,
25-OCT-2004 (TrEMBLrel. 28,
Albumin (Fragment).
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                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
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                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
67 kDa serum albumin (Alb-1) (Fragment).
67 kDa serum albumin (Alb-1) (Fragment).
68 serum sorripta (Red-eared slider turtle) (Pseudemys scripta).
69 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
70 Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
                                                                                                                                                                                                                                                                                                                                                        . .) (Potential)
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Allergen; Copper; Direct protein sequencing; Lipid-binding;
Metal-binding; Repeat; Signal.
1 18
PROPEP 19 23
CHAIN 24 615 Serum albumin.
DOMAIN 24 615 Albumin 1.
DOMAIN 20 Albumin 1.
DOMAIN 20 Albumin 1.
DOMAIN 408 599 Albumin 3.
                                                                                                                                                                                                                                                                                                                                                                                                            65.9%; Score 81; DB 1; Length 615;
                                                                                                                                                                                                                                                                                                                                                                                 ES9E4BBCAEC066C6 CRC64;
                                                                                                        Copper (By similarity).
By similarity.
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4; Mismatches
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HKSEIAHRYNDLKEETFKAVAM 51
                                                                                                                                                                                                                                                                                                                                                                                  69918 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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P81188;
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Pfam; PF01047; MarR;
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P83729;
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SEQUENCE
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NF41_NAEFO
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STRAIN=2603 V/R / Serotype V;
STRAIN=22229898; PubMed=12200547; DOI=10.1073/pnas.182380799;
Tettelln H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N., Messels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.E., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
    Gaps
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Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).

-!- SIMILARIY: Contains 1 HTH marR-type DNA-binding domain.

EMBL; AE014207; AAM99249.1; -.

TIGR; SAG014207; AAM99249.1; -.

GO; GO:0005522; C:intracellular; IEA.

GO; GO:0005322; C:intracellular; IEA.

GO; GO:0005325; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000855; Wing_hlx_DNA_bnd.
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  Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein gab0330.
OrderedLocusNames-gab0330;
Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation.
SEQUENCE 144 AA; 16656 MW; 465EAE2ABBF8DB34 CRC64;
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Last annotation update)
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Complete proteome; DNA-binding; Transcription;
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4; Mismatches
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OrderedLocusNames=SAG0343;
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                                         3 HKSEVAHRFKDLGEENFKALVL 24
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HKSEIAHRYNDLKEETDKAVXM 25
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Matches 12; Conservative
  13; Conservative
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NCBL_TaxID=216495;
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01-MAR-2003
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QBELLI
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STRAIN=NEW116 / Serctype III;
MEDLINE=2224508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek I., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
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NCBI_TaxID=5763;
                                                                                                                      "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513 (2002).
-!- SIMILARITY: Contains 1 HTH marR-type DNA-binding domain.
EMBL; AL766844; CAD45975.1;
-- Sagalist; pbs0330;
-- GO; GO:000552; C:intracellular; IEA.
GO; GO:000552; C:intracellular; IEA.
GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000855; Wing_hlx_DNA_bnd.
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Pred. No. 0.071;
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SEQUENCE 144 AA; 16656 MW; 465EAE2AB8F8DB34 CRC64;
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Last sequence update)
Last annotation update)
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SMART; SM00347; HTH MARR; 1.
Complete proteome; DNA-binding; Transcription;
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29-MAR-2004 (Rel. 43, Last sequence update)
29-ULI-2004 (Rel. 44, Last annotation update)
Unknown protein NF041 from 2D-PAGE (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 AA.
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(TrEMBLrel. 26, I
(TrEMBLrel. 26, I
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| DTHKSEIAHRQPDLG 15
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NCBI_TaxID=10090;
      NON CONS
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DOMAIN
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SEQUENCE
                                                           Query Match
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                                                                                                                                       RESULT 39
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                                                                 Appl. Bioinformatics 2:897-S107(2003).

-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water. Ca(2+), Na(+), K(+), fatty acids, binding capacity for water. Ca(2+), Na(+), K(+), fatty acids, hormones, bilitubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SIBCELLUIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Plasma.
-!- SIBCELLUIARITY: Palongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-!- SIMILARITY: Contains at least 2 albumin domains.
InterPro; IPRO00264; Serum albumin.
PROSITE; PS00212; Albumin, PARTIAL.
                                                                                                                                                                                                                                                                                                            Gapa
                         Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.
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                                                                                                                                                                                                                                                                                                            5; Indels
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Metcalf V., Brennan S., George P.;
"Using serum albumin to infer vertebrate phylogenies.";
Appl. Bioinformatics 2:897-8107(2003).
                                                                                                                                                                                                                                                                          548 AA; 63212 MW; D88DB41F238B8B8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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 TWO-COMPONENT SENSOR
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Pfam; PP02518; HATPase c; 1.
PRINTS; PR00344; BCTRLSENSOR.
PROSITE; PS50109; HIS_KIN; 1.
                                   Helicobacteraceae; Wolinella.
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Best Local Similarity 66.7°
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                   Wolinella succinogenes
                                                             SEQUENCE FROM N.A.
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                                           NCBI_TaxID=844;
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P83517;
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DOMAIN
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STRAIN=C57BL/6J; TISSUE=Thymus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS'BL/66; TISSUE=Thymus; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Carninci P., Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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STRAINS-CSTBLAIL/6J; TISSUE=Thymus;
STRAINS-CSTBL/6J; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Samamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kaphiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,
Voneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
length enriched library, clone:C920028B14 product:albumin 1, full
insert sequence. (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                           47.2%; Score 58; DB 1; Length 101;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRARIE-GSTBL/60; TISSUE-Thymus;
MEDILINE-21.085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM COMBORTIUM;
      4 4 Copper (By similarity).
28 29 81 81 81 81 81 9101 Albumin 2.
101 101 101 101 A51669C76226CC43 CRC64;
Copper (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 AA.
                                                                                                                                                                                                                                                                        Pred. No. 1;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                              3 HKSEVAHRFKDLGEENFKALVL 24
                                                                                                                                                                                                                                                                                                                                                                                                       ||| : |: :|| || ::|
HKSNICKHFQVVGEEKFKNIIL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
                                                                                                                                                                                                                                                                        45.5%;
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

Rukuda S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaukawa T.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koya S.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Saito H., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Saitoh H., Shinagawa A., Shiraki T., Sogabe Y., Tangami M.,

Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AKOSO644; BAC34360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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"Prediction of the coding sequences of mouse homologues of KIAA gene:
III. the complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones DNA Res. 10:167-180(2003).

EMBL; AK129208; BAC98018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Embryonic tail;
PubMed=14621295;
Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 2; Length 576;
Pred. No. 13;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     576 AA; 65002 MW; F85733E99AE37F04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 AA; 61568 MW; 57480E18D57ED6BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:87991; Albl.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR001703; Alphafetoprot.
InterPro; IPR000264; Serum albumin.
Pfam; PF00273; Serum albumin; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0803; APETOPROTEIN.
PRINTS; PRO0802; SERUMALBUNIN.
PPODOM: PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000504; RNA_rec_mot.
Beam; PR00006; RRM 1; 2.
SWART; SM00360; RRM; 3.
PROSITE; PS50102; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00212; ALBUMIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.5%;
62.5%;
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05-UUL-2004 (TrEWBLrel. 27, C
05-UUL-2004 (TrEWBLrel. 27, I
05-UUL-2004 (TrEWBLrel. 27, I
MXIAA0765 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 HRFKDLGEENFKALVL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|: ||||::|| |||
1 NRYNDLGEQHFKGLVL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 62.5
tes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=mKIAA0765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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062053
AC Q62053
AC Q6205
DT 05-JU
DT 
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    RTT REPRESENT TO THE SERVICE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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      Query Match
      43.1%; Score 53; DB 2; Length 569;

      Best Local Similarity 56.5%; Pred. No. 35;
      Aatches 13; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

      Qy
      1 DAHKSEVAHRFKDLGEENFKALV 23

      Db
      508 DAHKSEHLHRKKLNGREAFVHIV 530
```

Search completed: August 19, 2005, 10:55:34 Job time : 58 8ecs

Tue Aug 23 10:25:12 2005

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

- protein search, using sw model protein ĕ

August 19, 2005, 10:49:44; Search time 16 Seconds (without alignments) 144.325 Million cell updates/sec Run on:

US-09-846-328B-1\_COPY\_2\_25

1 DAHKSEVAHRFKDLGEENFKALVL 24 BLOSUM62 Gapop 10.0 , Gapext 0.5 score: Scoring table: Sequence:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 DB seq DB seq Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: Pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	* Query Match Length	DB	ID	Description
				1		•
п	123	100.0		٦	ABHUS	albumin
7	110	89.4	9	~	A47391	
e	108	87.8	607	н	ABBOS	serum albumin prec
4	106	86.2	608	-	ABRTS	
S	105	85.4	607	Н	ABSHS	
9	100	81.3	607	Н	ABHOS	serum albumin prec
7	97	78.9	605	Н	ABPGS	serum albumin prec
60	97	78.9	608	~	S57632	serum albumin prec
o	97	78.9	609	~	JC5838	albumin - Mongolia
10	92	74.8		~	S29749	serum albumin - do
11	89	72.4	30	~	B61511	serum albumin, mil
12	81	65.9	615	Н	ABCHS	serum albumin prec
13	20	40.7	67	8	T12251	sucrose synthase (
14	20	40.7	384	~	G85895	
15	50	40.7	384	~	C91051	
16	20	40.7		~	D65028	hypothetical 43.1
17	49	39.8		~	A53361	thyroxine-binding
18	49	39.8		~	856295	SAP155 protein - y
19	48	39.0		7	T20006	hypothetical prote
20	48	39.0	222	7	A97575	hypothetical prote
21	48	39.0		~	AI2795	conserved hypothet
22	48	39.0		-	VYHUD	vitamin D-binding
23	47.5	38.6		~	T06675	hypothetical prote
24	47	38.2		~	AB0230	probable exported
25	47	38.2	313	N	E83095	conserved hypothet
56	47	38.2	719	~	F96577	hypothetical prote
27	46.5	37.8	451	~	F89130	protein F52E1.10 [
28	46	37.4	180	~	T44944	hypothetical prote
29	46	37.4	220	0	B72219	ribulose-phosphate

probable TraD conj hypothetical prote	hypothetical prote	NA+/H+ antiporter	probable na+/h+ an	conserved hypothet	UTP-glucose glucos	cysteine proteinas	carbon monoxide de	DNA gyrase subunit	saframycin Mx1 syn	hypothetical prote	outer membrane lip	sucrose synthase (	hypothetical prote	probable sensor/re
G95324	856055	G64667	H71848	AD0822	841952	A45565	A97208	C82860	T18552	A48412	A49235	S29242	T18642	н83132
0.0	۰ م	~	N	N	~	7	7	7	~	~	N	N	~	7
79	314	383	383	388	394	441	639	814	2605	227	365	807	1161	1417
36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	35.8	35.8	35.8	35.8	35.8
<b>4.</b> 4.	ւ 4. Մ Ը	45	45	45	45	45	45	45	45	44	44	44	44	44
30	35	33	34	35	36	37	38	39	40	41	42	43	4	45

## ALIGNMENTS

_		
ESULT	SUHE	

- human [validated] serum albumin precursor

Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cibate: 29-Jul-1981 #sequence\_revision 31-Jan-1997 #text\_change 09-Jul-2004
Cibate: 29-Jul-1981 #sequence\_revision 31-Jan-1997 #text\_change 09-Jul-2004
Cibate: 29-Jul-1981 #sequence\_revision 139286; IS9313; G01747; SS5314; A91420; S06422; S366
Rilawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Seeburg
Rilawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Seeburg
Alticle: The sequence of human serum albumin cDNA and its expression in Escherichia coli
A;Reference number: A93743; MUID:82081882; PMID:6171778

A; Accession: A93743

A; Molecule type: mRNA A; Residues: 1-419.7K', 421-609 <LAW> A; Residues: 1-419.7K', 421-609 <LAW> A; Cross-references: UNIRROT: P02768; EMBL: V00495; GB:J00078; GB:L00132; GB:L00133; NID:g28 R; Dugaiczyk, A.; Law, S.W.; Dennison, O.E. R; Dugaiczyk, A.; Law, S.W.; Dennison, O.E. A; Dugaiczyk, A.; Law, S.W.; S.A. 79, 71-75, 1982 A; Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA. A; Reference number: A93936; MUID:82105994; PMID:6275391

A; Accession: A93936
A; Accession: A93936
A; Molecule type: mRNA
A; Residues: 1-120, G', 122-609 < DUG>
A; Cross-references: ENBL: V00494; NID: 928589; PIDN: CAA23753.1; PID: 928590
A; Cross-references: ENBL: Sakai, M.; Tamaoki, T.
J. Biol. Chem. 261, 3244-3251, 1986
A; Title: The human albumin gene. Characterization of the 5' and 3' flanki
A; Reference number: 139427; MUID: 86140099; PMID: 2419329

and 3' flanking regions and

,Accession: I39427

A;Status: translation not shown
A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-26 <URA>
A;Cross-references: GB:M13075; NID:g178330; PIDN:AAA51688.1; PID:g553173
A;Cross-references: GB:M13075; NID:g178330; M.; Minchiotti, L.; Putnam, F.W.
B;Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.
A;Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian family.
A;Reference number: 159286; MUID:94181575; PMID:8134387

A;Accession: I59286

A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residuse: 282-290, KSRFDLQ' < wAT>
A;Residuse: 282-290, KSRFDLQ' < wAT>
A;Cross-references: GB:S65192; NID:S546032; PIDN:AAB30282.1; PID:9546033
A;Cross-references: GB:S65192; NID:9546032; PIDN:AAB30282.1; PID:9546033
A;Note: this frame-shift variant, designated albumin Roma, leads to analbuminemia
R;Madison, J.; Galliano, M.; Matkins, S.; Minchiotti, L.; Porta, F.; Rosel, A.; Putnam, A;Matile: Genetic variants of human serum albumin in Italy: point mutants and a carboxyl-A;Reference number: 159313; MUID:9429404; PMID:8022807

A, Accession: I59313

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 589-590,'ALPRRVKNLLLQVKLP' <MAD> A;Cross-references: GB:S70799; NID:g547231; PIDN:AAB31177.1; PID:g547232

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F;29-202/Domain: serum albumin repeat homology <SAl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atase activity
A;Note: this frame-shift variant is designated albumin Bazzano; four additional variants R;Memaya_J. 'p Parrilla, R: Ayuso, M.S. submitted to the EMBL Data Library, March 1995
A;Reference number: G08292
A;Recession: G0174
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-120, 'George, P.M.; Peach, R.J.; Brennan, S.O.
B;Cooss-references: BMBL-1235, 1995
A;Ttoss-references: BMBL-1235, 1995
A;Ttoss-references: BMBL-1235, 1995
A;Ttoss-references: S5314
A;Molecule type: processing of recombinant proalbumin variants by the yeast Kex2
A;Reference number: S5314
A;Molecule type: procein
A;Residues: 19-27 cLED-
B;Molecule type: procein
A;Residues: 19-27 cLED-
A;Accession: A313, 1975
A;Accession: A31420
A;Attle: Complete amino acid sequence of human serum albumin.
A;Residues: 25-111, 'SC, 120-154, 'O., 156-193, 'E., 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-A', 1711: Isolation and structure elucidation of middle-molecular weight peptides from ur A;Reference number: S06422
A;Note: this paper is in German, with an English abstract
A;Reference number: S06422
A;Note: this paper is in German, with an English abstract
A;Reference procein
A;Reference number: S06422
A;Note: this paper is in German, with an English abstract
A;Reference number: B50822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S36882
A; Molecule type: protein
A; Rausler, E.; Spiteller, G.
A; Molecule type: protein
A; Residues: 45-67;411-160;311-337;469-490;570-581 <FIN>
R; Kausler, E.; Spiteller, G.
Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
A; Title: Bruchstuecke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmol
A; Reference number: S17599; MUID:92126241; PMID:1772598
A; Molecule type: protein
A; Residues: 25-54;354-357,431-447 <KAU>
A; Molecule type: protein
A; Residues: 25-54;354-357,431-447 <KAU>
A; Molecule type: protein
A; Residues: 25-54;354-357,431-447 <KAU>
A; Molecule type: protein
A; Reference number: A45800; MUID:89341406; PMID:2474609
A; Mille: Structures of histamine-releasing peptides formed by the action of acid proteas
A; Molecule type: protein
A; Residues: 166-173 <CAR>
A; Molecule type: Drotein
A; Residues: 166-173 <CAR>
A; Molecule type: Drotein
A; Residues: 166-173 <CAR>
A; Title: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-tre
A; Reference number: A03239; MUID:86242180; PMID:3087352
A; Title: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-tre
A; Reference number: A03239; MUID:86242180; PMID:3087352
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A;Residues: 166-173'L' <MOG>
R;Galliano, M.; Minchiotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, N. (Mathiotti, L.) 8721-8725, 1990
A;Title: Matations in genetic variants of human serum albumin found in Italy.
A;Reference number: A38255; MUID:91062352; PMID:2247440
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A; Title: Mass spectrometric identification of modifications A; Reference number: $36882; MUID:93384321; PMID:8373198
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A,Molecule type: protein
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A, Residues: 82-105, 'K', 107-110 <GAL2>
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A;Residues: 76-111 <GAL1>
A;Accession: B38255
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A,Residues: 76-83,'K',85-106 <GAL3>
A,Note: this variant is designated albumin Torino
R,Minchiotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
Eur. J. Biochem. 214, 437-444, 1993
Eur. J. Biochem. 214, 437-444, 1993
A,Title: The structural characterization and bilirubin-binding properties of albumin Hert
A,Reference number: S33298; WUID:93292504; PMID:8513793
A,Accession: S33298
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A; Molecule type: 55-261, 1265-281 (MINI)
A; Molecule this variant is designated albumin Herborn
A; Note: this variant is designated albumin Herborn
B; Minchiotti, L.; Galliano, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Porta,
Biochim. Bjophys. Acta III9, 232-238, 1992
A; Fitle: Two alloalbumins with identical electrophoretic mobility are produced by differe
A; Reference number: S21078; MUID:92190239; PMID:1347703
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Biochem. J. 171, 453-459, 1978
A;Title: Ligine residue 240 of human serum albumin is involved in high-affinity binding c
A;Title: Ligine residue 240 of human serum albumin is involved in high-affinity binding c
A;Reference number: A90299; MUID: 8186630; PMID: 656055
A;Contents: annotation; bilirubin-binding site
B;Peters, T: Reed, R.G.
A;Title: Serum albumin: conformation and active sites.
A;Title: Serum albumin: conformation and active sites.
A;Contents: annotation; binding sites
B;Harper, M.E.; Dugaiczyk, A.
Am. J. Hum. Genet. 35, 565-572, 1983
A;Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein genes
A;Contents: annotation; gene position
A;Contents: annotation; gene position
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Figureshies annotation, some process.

Figureshies annotation are found albumin is modified by acetylealicyclic acid. A, Fittle: Lygaine residue 199 of human serum albumin is modified by acetylealicyclic acid. A, Reference number: A46755; MUID:76257808; PMID:955075

A, Contents: annotation annotation acetyl group from aspirin (acetylealicyclic acid) A, Robnes, J. P.; Ponda, M.L.; Feldhoff, R.C.

FEBS Lett. 298, 266-268, 1992

A, Fittle: Identification of Lyg(190) as the primary binding site for pyridoxal 5'-phosphat A, Reference number: A56294; MUID:92183881; PMID:1544460

A, Contents: annotation

A, Contents: annotation and the primary phosphate to lygine-214 is described; in plants annotation and the primary process and the primary phosphate to lygine-214 is described; in plants and the primary process and the process and the primary process and the primary process and the p
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C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; phosphoprotein; plasma; pyridox:
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-609/Product: serum albumin #status experimental <MPT>
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A; Contents: annotation; three-dimensional structure and disulfide bonds
R; Saber, M.A.; Stockbauer, P.; Moravek, L.; Meloun, B.
Collect. Czech. Chem. Commun. 42, 564-579, 1977
A; Title: Disulfide bonds in human serum albumin.
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A;Accession: A91258
A;Molecule type: protein
A;Residues: 1-32 <MMG>
K;Hsisteh, O.C.; Linn, F.P.; Tam, M.F.
Anal. Biochem. 170, 1-8, 1988
A;Title: Blectroblotting onto glass-fiber filter from an analytical isoelectrofocusing ge
A;Reference number: A60808; WUID:88267456; PMID:3389500
                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 25-41 <HSI>
R;Strawich, E.; Glimcher, M.J.
Bur. J. Blochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albun
A;Reference number: S10780; MUID:90336641; PMID:2379503
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A; Residues: 25-41,'H',43-57,59-64 <STR>
R; Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J: Immunol. 143, 1660-1684, 1989
A; Title: Structures of histamine-releasing peptides formed by the action of acid protease
A; Reference number: A45800; MUID:89341406; PMID:2474609
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A;Molecule type: protein
A;Residues: 163-172 <CAR>.
R;Carraway, R.E.; Mitra, S.P.; Cochrane, D.E.
J. Biol. Chem. 262, 5968-5973, 1987
A;Title: Structure of a biologically active neurotensin-related peptide obtained from per
A;Reference number: A26693; MUID:87194805; PMID:2437111
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A;Residues: 25-41,'H',43-117,'EQ',120-179,181-189,'E',191-194,'A',196-213,'T',215-288,'B
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A; Reference number: A91457
A; Contents: annotation; disulfide bonds
R; Werlen, R.C.; Offord, R.E.; Rose, K.
R; Werlen, R.C.; Offord, R.E.; Rose, K.
A; Title: Preparation and characterization of novel substrates of insulin proteinase (EC A); Reference number: S55232; MUID:95031935; PMID:7945219
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A; Residues: 529-516; 569-572 < WER>
A; Residues: 529-516; 569-572 < WER>
C; Superfamily: serum albumin serum albumin repeat homology
C; Superfamily: serum albumin; serum albumin sexperimental < SIG>
F; 19-24 | Domain: signal sequence #status experimental < PRO>
F; 19-24 | Domain: propeptide #status experimental < PRO>
F; 25-607 | Product: serum albumin #status experimental < MPT>
F; 25-201 | Domain: serum albumin repeat homology < SA1>
F; 220-337 | Domain: serum albumin repeat homology < SA2>
F; 210-337 | Domain: serum albumin repeat homology < SA3>
F; 210-337 | Domain: serum albumin repeat homology < SA3>
F; 210-351 | Domain: serum albumin repeat homology < SA3>
F; 210-351 | Domain: serum albumin repeat homology < SA3>
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A, Residues: 165-172, 'L' <CA2>
R, Reed, R.G., Putnam, F.W.; Peters Jr., T.
Ajochem. J. 191, 867-868, 1980
A,Title: Sequence of residues 400-403 of bovine serum albumin.
A, Reference number: A90309; MUID:82023364; PMID:7283978
A; Reference number: A91258; MUID:80024278; PMID:488109
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A;Title: Structure of bovine serum albumin.
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A;Reference number: A94551
A;Accession: A94551
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A; Residues: 402-433 < REE>
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A; Residues: 190-195 < BR2>
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A Molecule type: mRNA; protein
A; Molecule type: mRNA; protein
A; Molecule type: mRNA; protein
A; Molecule: 1-600 < MALY
A; Cross-references: UNIPROT: Q28522; GB:M90463; NID:g342294; PIDN: AAA36906.1; PID:g342295
A; Cross-references: UNIPROT: Q28522; GB:M90463; NID:g342294; PIDN: AAA36906.1; PID:g342295
A; Cross-references: UNIPROT: G28525; GB:M90463; NID:g342294; PIDN: AAA36906.1; PID:g342295
A; Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBIP:128281)
C; Superfamily: serum albumin; serum albumin repeat homology <SA1>
F; 21-194 / Domain: serum albumin repeat homology <SA3>
F; 405-584 / Domain: serum albumin repeat homology <SA3>
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C;Species: Marcaca mulatta (rhesus macaque)
C;Dates: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Dates: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Matchins, G; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam, F. Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
A;Title: CDNA and protein sequence of polymorphic macaque albumins that differ in biliru A;Reference number: A47391; MUID:93211971; PMID:8460152
                                     F;221-394/Domain: serum albumin repeat homology <5A2>
F;413-592/Domain: serum albumin repeat homology <5A3>
F;47/Shiding site: copper (His) #status predicter
F;77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393,°
F;71-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,serimental
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A;Residues: 25-41,"+/,43-189,"E',191-213,"T',215-323,'D',325-393,'TS',396-607 <HIR>
K;MacGillivray, R.T.A.; Chung, D.W.; Davie, E.W.
Eur. J. Blochem. 98, 477-485, 1979
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A;Title: Biosynthesis of bovine plasma proteins in a cell-free system
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                P;166-174/Product: kinetensin #status experimental <KIP>
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ilarity 87.5%;
Conservative
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Best Local Similarity 79.2%;
Matches 19; Conservative
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llarity 79.2%;
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nes 19; Conserv
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A; Residues: 1-607 <BRO>
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A;Reference number: A91946; MUID:78109429; PMID:564345
A;Aritle: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage
A;Aritle: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage
A;Modecule type: protein
A;Modecul
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A; Residues: 1-608 <SAR>
A; Residues: 1-608 <SAR>
A; Residues: 1-608 <SAR>
A; Coss-references: UNIPROT: P02770; GB: V01222; GB: J00698; NID: G55627; PIDN: CAA24532.1; F A; Cross-references: UNIPROT: Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
B; Diol. Chem. 252, 6846-6855, 1977
A; Title: Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece. Analys A; Reference number: A2211; MUID: 77249657; PMID: 893447
A; Note: cleavages during protein maturation
F;77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,
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C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
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                                                                                                87.8%; Score 108; DB 1; Length 607;
83.3%; Pred. No. 7.2e-08;
ive 1; Mismatches 3; Indels
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                                                                                                                                                                                                                  20; Conservative
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                                                                                                                 Query Match
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F;777.86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393,41
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F;412-591/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
F;77/Binding site: Dilirubin (192, 191-200, 223-269, 268-276, 288-302, 301-312, 339-384, 383-392, 41
F;263/Binding site: bilirubin (Lys) #status predicted
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Eur. J. Biochem. 215, 205-212, 1993
A,Fitele: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nm 1
A,Reference number: S34053; MUID:93345495; PMID:8344282
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A;Residues: 1-607 <HOA>
A;Cross-references: UNIPROT: P35747; GB:X74045; NID:g399671; PIDN: CAA52194.1; PID:g399672
A;Cross-references: UNIPROT: P35747; GB:X74045; NID:g399671; PIDN: CAA52194.1; PID:g399672
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, I teroid hormones (weak bonds with these hormones promote their transfer across the membrar teroid hormones (weak bonds with these hormones promote their transfer across the membrar C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S06936
R;Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10455, 1989
A;Fitle: Nucleotide and deduced amino acid sequence of sheep serum albumin.
A;Reference number: S06936; MUID:90098889; PMID:2602160
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Serum albumin precursor - domestic horse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO-
F;25-607/Product: serum albumin #status predicted <MAT>
F;29-201/pomain: serum albumin repeat homology <SAI>
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F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-608/Product: serum albumin #status experimental <MAT>
F;29-202/Domain: serum albumin repeat homology <SA1>
F;221-394/Domain: serum albumin repeat homology <SA2>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;217/Binding site: copper (His) #status experimental
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Pred. No. 2e-07;
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A;Molecule type: mRNA
A;Residues: 1-608 <HI2>
A;Cross-references: UNIPROT:P49064; EMBL:X84842; NID:g886484; PIDN:CAA59279.1; PID:g8864f
                                                                                                                                                                                                             A Experimental Source: liver
C;Comment: This protein is the major protein component in plasma. It functions as a multi-
C;Comment: This protein is the major protein component in plasma. It functions as a multi-
c;Comment: This protein is the major protein component in plasma.
C;Superfamily: serum albumin; serum albumin; serum albumin predicted <SIG>
C;Superfamily: serum albumin #status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <NRP>
F;25-668/Product: serum albumin #status predicted <MAT>
F;29-202/Domain: serum albumin repeat homology <SA1>
F;21-394/Domain: serum albumin repeat homology <SA3>
F;413-592/Domain: serum albumin repeat homology <SA3>
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A,Title: Sequencing of CDNA encoding serum albumin and its extrahepatic synthesis in the
A,Reference number: JC5638; MUID:98116663; PMID:9455485
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A)Reference number: JC4660; MUD:96194824; PMID:8647469
A)Ancession: JC4660
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C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JC5838
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C;Superfamily: serum albumin; serum albumin repeat homology
F;222-395/Domain: serum albumin repeat homology <SA2>
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70.8%; Pred. No. 2.9e-06;
tive 5; Mismatches 2;
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78.3%; Pred. No. 2.9e-06;
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Pred. No. 5.7e-07;
6; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Yoshida, K.; Seto-Ohshima, A.; Sinohara, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||:||:||:|||
EAHQSEIAHRFNDLGEEHFRGLVL 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AHKSEVAHRFKDLGEENFKALVL
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Best Local Similarity 66.7
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            albumin - Mongolian jird
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-609 < YOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JC5838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S29749
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A; Residues: 23-51, 'X', 53-54, 'XXXGY', 146, 'E', 148, 'E', 150-151, 'XVN', 155 < LIM>
A; Residues: 23-51, 'X', 53-54, 'XXXGY', 146, 'E', 148, 'E', 150-151, 'XVN', 155 < LIM>
A; Note: albumin and other dental ename!
A; Note: albumin and other erum proteins are also found in bone
C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
Leroid hormones (weak bonds with these hormones promote their transfer across the membra
C; Superfamily: serum albumin; serum albumin repeat homology
C; Keywords: carrier protein; duplication; metal binding; plasma
F; 11-16/Domain: signal sequence (fragment) # status predicted < SIG>
F; 71-22, Domain: serum albumin repeat homology < SA1>
F; 21-39/Domain: serum albumin repeat homology < SA2>
F; 21-30, Domain: serum albumin repeat homology < SA3>
F; 10-39, Domain: serum albumin repeat homology < SA3>
F; 10-39, Domain: serum albumin repeat homology < SA3>
F; 10-39, Domain: serum albumin repeat homology < SA3>
F; 10-16, Binding site: bilirubin (Lys) # status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S01382
A;Status: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule: 1-605 <MEI>
A;Cross-references: UNIPROT:P08835; EMBL:X12422; NID:g1875; PIDN:CAA30970.1; PID:g833798
R;Limeback, H.; Sakarya, H.; Chu, W.; Mackinnon, M.
B; Dane Miner: Res 4, 255-241, 1989
A;Title: Serum albumin and its acid hydrolysis peptides dominate preparations of mineral A;Reference number: A61006; MUID:89269769; PMID:2728927
A;Accession: A61006
A;Accession: A61006
                                             F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
F;29-24/Domain: propeptide #status predicted <WAT>
F;29-201/Domain: serum albumin repeat homology <SA1>
F;20-393/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
F;77-86,99-115,114-125,147-192,191-200,222-259,268-276,288-302,301-312,339-384,383-392,75,581/Anding site: bilirubin (Lys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berum albumin precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Daces 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S01382; Aslofo6
R;Welnstock, J; Baldwin, G.S.
Nucleic Acids Res. 16, 9045, 1988
A;Fitle: Nucleotide sequence of porcine liver albumin.
A;Reference number: S01382; MUID:89016582; PMID:3174440
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C;Species: Felis silvestris catus (domestic cat)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: JC4660; S57632
Gene 169, 295-296, 1996
Gene 169, 295-296, 1996
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75.0%; Pred. No. 2.9e-06;
iive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                        81.3%; Score 100; DB 1; ilarity 75.0%; Pred. No. 1.1e-06; Conservative 3; Mismatches 3
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Best Local Similarity 75.v.
Best Local 18; Conservative
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nes 18; Conserv
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Best Local
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S57632
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hypothetical protein yfgB (imported) - Escherichia coli (strain 0157:H7, substrain EDL93:
C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Accession: G85895
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousls, K.; Apodaca, Natitle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein EC83379 [imported] - Escherichia coli (strain O157:H7, substrain RIN C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: C91051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:08XAA4; GB:AE005174; NID:g12516911; PIDN:AAG57627.1; GSPDB:Gr
A,Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                        sucrose synthase (EC 2.4.1.13) - common ice plant (fragment)
C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 3-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T1251
R;Michalowski, C.B.; Bohnert, H.J.
R;Michalowski, C.B.; Bohnert, H.J.
R;Michalowski, C.B.; Bohnert, H.J.
A;Description: An expressed sequence tag for sucrose synthase from M. crystallinum.
A;Reference number: Z17473
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A,Residues: 1-67 «MIC»
A,Cross-references: UINPROT:O65179; EMBL:AF054446; NID:93064040; FID:93064041
C,Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase
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65.9%; Score 81; DB 1; Length 615; 63.6%; Pred. No. 0.00063; rive 4; Mismatches 4; Indels
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Pred. No. 2.1;
3; Mismatches 5; Indels
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                                                                                                                                                                                                                30 HKSEIAHRYNDLKEETFKAVAM 51
                                                                                                                                                                   3 HKSEVAHRFKDLGEENFKALVL 24
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22 DLNRQQMREFFKDLGEKPFRA 42
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Best Local Similarity 52.9%;
Matches 9; Conservative
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        Query Match
Best Local Similarity 63.65
Matches 14; Conservative
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Matches 9; Conserv
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A:Molecule type: DNA
A;Residues: 1-384 <STO>
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C91051
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A;Reference number: A13451; MUID:78019943; PMID:911327

A;Reference number: A13451

A;Reference number: A13451

A;Residues: 19-23, MY, 25-30 <ROS>

C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, mones (weak bonds with these hormones promote their transfer across the membranes), thyr C;Superfamily: serum albumin; derum albumin repeat homology

C;Superfamily: earum albumin; derum albumin repeat comology

C;Reywords: carrier protein; duplication; metal binding; plasma

F;19-16/Domain: signal sequence #status predicted <ROS

F;19-16/Domain: propeptide #status predicted <ROS

F;19-16/Domain: propeptide #status predicted <ROS

F;19-16/Domain: propeptide #status predicted <ROS

F;10-16/Domain: predicted *ROS

F;10-16/Domain: predicted *ROS

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A; Residues: 1-615 <CAS.
A; Creatings: 1-615 <CAS.
A; Creating R. J. G.; Wiskocil, R.; Vasa, M.; Roy, R.N.; Lau, P.C.K.; Deeley, R.G.
J. Biol. Chem. 258, 4556-4564, 1983
A; Title: The S' noncoding and flanking regions of the avian very low density apolipoprot
A; Reference number: A05078; MUID:83161037; PMID:6187737
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F;27-613/Product: serum albumin repeat homology <SA1>
F;25-398/Domain: serum albumin repeat homology <SA2>
F;415-398/Domain: serum albumin repeat homology <SA3>
F;417-596/Domain: serum albumin repeat homology <SA3>
F;410/Binding site: copper (His) #status predicted
F;80-89;102-118,117-128,152-197,196-205,228-274,273-281,293-307,306-317,344-389,388-397,
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                                                                                                                                                                                                                                                                                 Gerum albumin, milk-derived - Australian echidna (fragment)
C;Species: Tachyglossus aculeatus (Australian echidna)
C;Species: Tachyglossus aculeatus (Australian echidna)
C;Accession: B61511
R;Teahan, C.G.; McKenzie, H.A.; Griffiths, M.
Comp. Blochem. Physiol. B 99, 99-118, 1991
A;Titles some monotreme milk "whey" and blood proteins.
A;Title: Some monotreme milk "whey" and blood proteins.
A;Accession: B61511
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-30 cGRI>
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Cispecies: Gallus gallus (chicken)
Cibate: 31-Dec.1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
Cibaccession: S15571; A05078; Ā13451
R;cassady, A.I.; Salklld, C.K.; Baverstock, P.; Wallace, J.C.
submitted to the EMBL Data Library, July 1991
A;Reference number: S15571
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Biochem. Biophys. Res. Commun. 78, 1060-1066, 1977
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C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: milk
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                    24
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                        DAHKSEVAHRFKDLGEENFKALVL
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A; Residues: 1-28 < HAC>
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C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence revision 19-Oct-1995 #text_change 20-Jun-2000
C;Accession: S56295; S62251; S63787
C;Accession: S56295; S62251; S63787
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanun
submitted to the EMBL Data Library, May 1995
A;Description: Analyais of the nucleotide sequence of chromosome VI from Saccaromyces ceì
A;Reference number: S56186
A;Accession: S56295
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R;EK4, T.; Nattou, M.; Hagiwara, H.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Ksast 12, 149-167, 1996
A;Title, Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome V A;Reference number: S63787; MUID:96287652; PMID:8686379
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                                                   A;Molecule type: protein
A;Residues: 1-30;31-45;46-66;67-74;75-84;85-94;95-109;110-122;123-138;139-153 <LIW>
C;Keywords: plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C47E12.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross references: EMBL:D50617; NID:g836685; PID:g836795; MIPS:YFR040w R;Murakami, Y. submitted to the EMBL Data Library, December 1994
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A;Reference number: Z19210
A;Accession: T20006
A;Acstant: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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N,Alternate names: protein R013; protein YFR040w
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A;Map position: 6R
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                                                                                                                                                                                                Score 49;
Pred. No.
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442 HENQLHEKFKPLGFERFKVVEL 463
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Best Local Similarity 33.3%;
Matches 8; Conservative
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A, Accession: S62251
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Best Local Similarity
Matches 9; Conserv
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A;Residues: 1-905 <MUR>
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           A;Accession: S41664
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C;Species: L2-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: D65028
C;Accession: D65028
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Ttle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A44720; MUID:97426617; PMID:9278503
A;Accession: D65028
A;Accession: D65028
A;Accession: D65028
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-384 cBLAT>
               S.
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A,Experimental source: strain K-12, substrain MG1655
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A,Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Title: Structure of a reptilian plasma thyroxine binding protein indicates homology
A;Reference number: S41664; MUID:94161555; PMID:8117112
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterchemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C91051
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-384 <HAX>
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A;Gene: EC83379
C;Superfamily: conserved hypothetical protein HI0365
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A;Gene: y£gB
C;Superfamily: conserved hypothetical protein HI0365
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DLNRQQMREFFKDLGEKPPRA 42
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DLNRQQMREFFKDLGEKPFRA 42
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-431, 'E', 433-435, 'T', 437-474 < WIT>
A;Residues: 1-431, 'E', 433-435, 'T', 437-474 < WIT>
A;Cross-references: GB:LiDo41; NID:g340281; PIDN:AAA61704.1; PID:g639896
A;Experimental source: allele Gc1
R;Yang, F.; Naberhaus, K.H.; Adrian, G.S.; Gardella, J.M.; Brissenden, J.E.; Bowman, B.H. Gene 54, 285-290, 1987
A;Title: The vitamin D-binding protein gene contains conserved nucleotide sequences that A;Reference number: A29096; MID:88005794; PMID:2958390
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-19 < YAN2>
A; Cross-references: GB:M17156; NID:g181489; PIDN:AAA19662.1; PID:g463096
R; Crocke, N.E.; David, E.V.
Clin. Invest. 76, 2420-2424, 1985
A; Title: Serum vitamin D-binding protein is a third member of the albumin and alpha fetor
A; Reference number: A92765; MUID:86086396; PMID:2416779
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A;Cross-references: UNIPROT:P02774; GB:X03178; GB:M11321; NID:g31675; PIDN:CAA26938.1; P1
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A;Cross-references: GB:S67480; NID:g455967; PIDN:AAB29423.1; PID:g455970
A;Cross-references: GB:S67480; NID:g455967; PIDN:AAB29423.1; PID:g455970
R;Schoencgen, F.; Metz-Boutigue, M. Hi.; Jolles, J.; Constans, J.; Jolles, P.
Biochim. Biophys. Acta 871, 189-198, 1986
A;Title: Complete amino acid sequence of human vitamin D-binding protein (group-specific A;Reference number: A24066; MUID:86216223; PMID:2423133
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R; Witke, W.F.; Gibbs, P.E.M.; Zielinski, R.; Yang, F.; Bowman, B.H.; Dugaiczyk, A. Genomics 16, 751-754, 1993
A; Title: Complete structure of the human Gc gene: differences and similarities between A; Reference number: A46759; MUID:93315171; PMID:8325650
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A, Residues: 1-167, E', 169-326, R', 328-431, E', 433-435, T', 437-474 <COO>
A, Residues: 1-167, E', 169-326, NID: 9181481; PIDN: AAAS2173.1; PID: 9181482
A, Experimental source: allele Gc1
R; Braun, A.; Kofler, A.; Morawietz, S.; Cleve, H.
B; Braun, Biophys. Acta 1216, 385-394, 1993
A; Title: Sequence and organization of the human vitamin D-binding protein gene.
A; Reference number: S39787; MUID: 94092730; PMID: 7505619
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                                                                                                                                                                                                                                                                                                                        vitamin D-binding protein precursor [validated] - human NyAlternate names: DBP; Gc-globulin; group-specific component C;Species: Hono sapiens (man) C;Species: Hono sapiens (man) C;Date: 28-May-1986 #sequence revision 28-May-1986 #text change 09-Jul-2004 C;Accession: A94076; A46759; $29096; A92765; S39787; A24066; A90427; A03237 R;Yang, F.; Brune, J.L.; Naylor, S.L.; Cupples, R.L.; Naberhaus, K.H.; Bowman, Proc. Natl. Acad. Sci. U.S.A. 82, 7994-7998, 1985 Aprille: Human group-specific component (Ge) is a member of the albumin family. A;Reference number: A94076; MUID:86068030; PMID:2415977
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Biochemistry 18, 1611-1617, 1979
A;Title: Molecular basis for the three major forms of A;Reference number: A90427; MUID:79145448; PMID:218624
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       7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein AGR_C_3280 [imported] - Agrobacterium tumefaciens (strain C58, Cere C_iSpeciaes agrobacterium_tumefaciens - Agrobacterium_tumefaciens - Agrobacterium_tumefaciens - C_iSpeciaes - Agrobacterium_tumefaciens - C_iSpeciaes - Agrobacterium_tumefaciens - C_iSpeciaes - Agrobacterium_tumefaciens - Agrobacterium, Agrodaner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Alinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97575
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: A12795
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A;Map position: circular chromosome
C;Superfamily: Neisseria meningitidis probable integral membrane protein NMA2020
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   A; Experimental source: clone C47E12
C; Genetics:
A; Gene: CESP: C47E12.9
A; Map position: 4
A; Introns: 25/3; 51/3; 115/3
C; Superfamily: Caenorhabditis elegans hypothetical protein C47E12.9
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Pred. No. 14;
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Pred. No. 12;
3; Mismatches
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A,Experimental source: strain C58 (Dupont)
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A Molecule type: DNA
A Residues: 1-222 <KUR>
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A;Residues: 1-222 <KUR>
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A, Map position:
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A;Molecule type: DNA
A;Residues: 1-313 <STO>
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A;Molecule type: DNA
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C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Accession: T06675

R;Quetier, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigu submitted to the Protein Sequence Database, April 1999

A;Reference number: Z15793

A;Accession: T06675

A;Accession: T0675

A;Accession: T0
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probable exported protein YPO1886 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0230

R;Parkhill, J.; Wren. B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                      A. Caross - references: GDB:119263; OMIM:139200
A. Caross - references: GDB:119263; OMIM:139200
A. Map position: 4q12-4q13
A. Introns: 20/1; 43/2; 81/3; 158/2; 202/3; 234/2; 277/3; 345/2; 388/3; 421/2; 465/3
A. Introns: 20/1; 43/2; 87/3; 158/2; 202/3; 234/2; 277/3; 345/2; 388/3; 421/2; 465/3
A. Introns: 20/1; 43/2; 87/3; 158/2; 202/3; 234/2; 277/3; 345/2; 388/3; 421/2; 465/3
C; Superfamily: serum albumin; gerum albumin repeat homology constraints experimental cMAL2>
F; 11-16/Domain: serum albumin repeat homology constraints
F; 26-199/Domain: serum albumin repeat homology constraints
F; 404-474/Domain: serum albumin repeat homology constraints
F; 404-474/Domain: serum albumin repeat homology constraints
F; 26-139, 286-130; 111-122, 145-130; 189-139; 220-266, 265-273, 286-300, 299-311, 335-376, 375
F; 288/Binding site: carbohydrate (Asn) (covalent) #status predicted
A;Residues: 17,'Q',19-21,'N',23-36,'XXX',40-41;472-474 <SVA>
C;Comment: DBP is a multifunctional protein found in plasma, ascitic fluid, cerebrospina nts polymerization of actin by binding its monomers. DBP associates with membrane-bound C;Comment: Over 80 variants of human DBP have been identified. The three most common all A;Gene: GDB:GC
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C;Superfamily: Arabidopsis thaliana disease resistance protein EDS1
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Pred. No. 49;
1; Mismatches 8; Indels
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Local Similarity 56.5%;
les 13; Conservative 1
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Best Local Similarity 41.7
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A; Status: preliminary
A; Molecule type: DNA
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A;Cross-references: UNIPROT:Q8ZF35; GB:AL590842; PIDN:CAC90702.1; PID:g15979905; GSPDB:GNC;Genetics:
A;Gene: YP01886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conserved hypothetical protein PA4420 [imported] - Pseudomonas aeruginosa (strain PAO1) C; Species: Pseudomonas aeruginosa (strain PAO1) C; Species: Pseudomonas aeruginosa (strain PAO1) C; Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 A; Stover, C.K.; Pham, X.O.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathoral A; Reference number: A82950; MUID:20437337; PMID:10984043
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73
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Pred. No. 17;
5; Mismatches
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ilarity 47.4%; Pred. No. 28;
Conservative 4; Mismatches
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C;Superfamily: Escherichia coli yabC protein
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Beg

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probable TraD conjugal transfer protein [imported] - Sinorhizobium meliloti (strain 1021)|
C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: 65524
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
R;Alman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.,
Proc. Natl. Acad. Sci. U.S.A. 98, 9889, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilots
A;Reference number: A95262; MUID:21396509; PMID:11481432
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A;Nolecule type: DNA
A;Residues: 1-79 «KUR»
A;Reperimental source: strain 1021, megaplasmid pSymA
R;Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Ps;Galibert, F.; Finan, T.M.; Lowis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 68-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.(A,Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:09X243; GB:AE001811; GB:AE000512; NID:g4982291; PIDN:AAD36784
A;Experimental source: strain MSB8
                                                                                              A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571
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C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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2; Mismatches
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60.0%; Pred. No.
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51 RLRDIGEEAFKAPAL 65
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Matches 9; Conservative
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Matches 9; Conserv
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A;Molecule type: DNA
A;Residues: 1-220 <ARN>
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                                                                                                                                                                                                                                                                                                                protein F52E1.10 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89130
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: F89130
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C;Species: Natronobacterium pharaonis
C;Date: 3-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44444
R;Mattar, S:; Engelhard, M.
Eur. J. Biochem. 250, 332-341, 1997
A;Title: Cytochrome ba3 from Natronobacterium pharaonis: An archaeal four-subunit cytoch A;Reference number: Z22876; MUID:98088958; PMID:9428682
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C;Species: Thermotoga maritima
C;bate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B7219
                                          Gaps
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                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
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A;Molecule type: DNA
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                                          1; Mismatches
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                52.4%; Pred. No.
                                                                                                                                                                  494 HKNGSLHDFLHLSEESKALV 514
                                                                                                       23
                                                                                                       3 HKSEVAHRFKDLGEENFKALV
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Best Local Similarity 48.1
Matches 13; Conservative
                                          11; Conservative
            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-451 <STO>
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                                          Matches
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probable na+/h+ antiporter - Helicobacter pylori (atrain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Reb-1999 #sequence_revision 12-Reb-1999 #text_change 09-Jul-2004
C;Accession: H71848
C;Accession: H71848
C;Accession: H71849
C;Accession: B. D. D. D. D. D. Mills, S. D. J. Jang, Q. J. Taylor, D. B. J. Vovis, G. F. J. Inces, C. J. Gibson, R. Macure 397, J76-180, 1999
A;Altle: Genomic sequence comparison of two unrelated isolates of the human gastric pathr A, Title: Genomic sequence A, Free MID: 99120557; PMID: 9923682
A, Accession: H71848
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Asture 413, 848-852, 201
A;Authors Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Attle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Gross-references: UNIPROT:092K33; GB:AE001538; GB:AE001439; NID:g4155697; PIDN:AAD0668
A.Experimental source: strain J99
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UTP-glucose glucosyltransferase - cassava (fragment)
C;Species: Manihot esculenta (cassava)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S41952
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C;Superfamily: conserved hypothetical protein HI0365
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69;
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53.8%; Pred. No. 69;
tive 3; Mismatches
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| DLNRQQMREFFKNLGEKPFRA 46
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254 HKSELIHKLNDVG 266
254 HKSELIHKLNDVG 266
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Matches 7; Conserv
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-388 <PAR>
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G64667

NA+/H+ antiporter - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: G64667

R;Tomb, J.E.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujli, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

N;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Attle: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-383 < TOM
A;Residues: 1-383 < TOM
A;Coss-references: UNIPROT:025795; GB:AE000624; GB:AE000511; NID:g2314340; PIDN:AAD0822
C;Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein YMR241w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein YM9408.03
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Species: Sacharomyces cerevisiae
R.Species: Sacharomyces cerevisiae
R.Species: Sacharomyces cerevisiae
R.Species: Sacharomyces
R.Species: Regulation
R.Species: Regu
    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-264 <MUR>
A;Cross-references: UNIPROT: 098230; EMBL: AL109848; PIDN: CAB52834.1; GSPDB: GN00070; SCOED
A;Experimental source: strain A3(2)
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Streptomyces coelicolor hypothetical protein SCI51.10c
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A;Crose-references: SGD:SO004854
A;Map position: 13R
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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                                                                                                                                                                                                                                                                                                                                                                               Query Match 36.6%; Score 45; DB 2; Length 264; Best Local Similarity 52.9%; Pred. No. 47; Matches 9; Conservative 3; Mismatches 5; Indels
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llarity 45.0%; Pred. No. 56;
Conservative 4; Mismatches
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180 VVARLKELGEASFRVLV 196
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nes 7; Conserv
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     1; Mismatches
                                                                                         383 AQADETAQRLIELGIENFK 401
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                                                     2 AHKSEVAHRFKDLGEENFK 20
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Local Similarity 55.6%;
hes 10; Conservative
     10; Conservative
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Best Local S:
Matches 10
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     Matches
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A,Gene: CAC2498
C,Superfamily: carbon-monoxide dehydrogenase, beta subunit; hybrid cluster [4Fe-2S-30]
R; Hughes, J.; Hughes, M.A.
submitted to the EMBL Data Library, January 1994
submitted to the EMBL Data Library, January 1994
sh Description: Multiple secondery plant product UDP-glucose glucosyltransferase genes
A; Reference number: S41950
A; Reference number: S41952
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-394
A; Cross-references: UNIPROT: Q40288; EMBL: X77463; NID: 9453250; PID: 9453251
C; Superfamily: flavonol 03-glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cysteine proteinase (BC 3.4.22.-) - Theileria annulata
Cysteine proteinase (BC 3.4.22.-) - Theileria annulata
Cysteis: Theileria annulata
Cysteis: Theileria annulata
Cystesion: Aspar. 20-Apr.1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
Cystession: Asp565
RyBaylis, H.A.; Megson, A.; Mottram, J.C.; Hall, R.
Mol. Biochem. Parasitol. 54, 105-107, 1992
A;Title: Characterisation of a gene for a cysteine protease from Theileria annulata.
A;Reference number: A45565; MUID:92389980; PMID:1518523
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A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: Hissar
A; Note: sequence extracted from NCBI backbone (NCBIN:112709, NCBIP:112710)
C; Superfamily: papain
C; Keywords: cysteine proteinase; hydrolase
F; 252, 381, 403/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1.441 < BAX>
A;Cross-references: UNIPROT:P25781; GB:M86659; NID:g161886; PID:g161887
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                                                                                                                                                                                                                                                                                                    2; Length 394;
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                    Score 45; DB
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             353 HHSEIRKRVKEMSDKSRKALM 373
                                                                                                                                                                                                                                                                                                                                                                                                              3 HKSEVAHRFKDLGEENFKALV 23
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52.6%;
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llarity 38.1%;
Conservative
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165 NKFSDLSDEEFKAL 178
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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A,Molecule type: DNA
A,Residues: 1-639 <KUR>
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Cibate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C82860
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-814 <SIM>A; Residues: 1-814 <SIM
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al Briones, M.R.S.; Bueno, M.R.D.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Fraga, J.S.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Muthors: Ferreira, V.C.A; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme A; Authors: Rerreira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lighter Chado, M.A.; Madeira, M.W.; Madeira, M.V.; Marco, B.E.; Martins, E. M.F.; Mateukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miracia, E.G.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; Ge Oliveira, M.C.; Goliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Silva, A.M.; Silva Jr., W.A.; de Silva, A.C.; Frighten, V.; Sawasaki, A; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Varjovski-Almeida, S.; Vettore, A.L.; Ze A; Contents: annotation
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A;Cross-references: UNIPROT:Q50858; EMBL:U24657; NID:g1171127; PID:g1171129; PIDN:AAC441; C;Genetics:
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C.Species: Table2
R.Species: Table2
R.Species: Table3

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DNA gyrase subunit B XF0005 [imported] - Xylella fastidiosa (strain 9a5c)
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Pred. No. 1.5e+02;
0; Mismatches 8; Indels
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C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
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C;Keywords: carrier protein
F;535-978/Domain: acetate-CoA ligase homology <ACL1>
F;997-1065/Domain: acyl carrier protein homology <ACP1>
F;1643-2091/Domain: acetate-CoA ligase homology <ACP2>
F;2110-2178/Domain: acyl carrier protein homology <ACP2>
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Query Match 36.6%; Score 45; DB 2; Length 2605; Best Local Similarity 46.7%; Pred. No. 4.9e+02; Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 DAHKSEVAHRFKDLG 15 ||| :::|| :|| Db 1629 DAHANQLAHHLRQLG 1643 Search completed: August 19, 2005, 10:58:46 Job time : 18 secs

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